

FIGURE 1

CTAAAAAAATATGTTCTCTACAACACCAAGGCTCATTAAAATATTTAAATATT
AATATACATTCTTCTGTCAGAAATACATAAAACTTATTATATCAGCGCAGG
5 GCGGCGCGCGTCGGTCCCAGGAGCAGAACCCGGCTTTCTTGGAGCGACG
CTGTCTCTAGTCGCTGATCCAAATGCACCGGCTCATCTTGTCTACACTCTA
ATCTGCGCAAACCTTGAGCTGTCGGACACTTCTGCAACCCCGCAGAGCG
CATCCATCAAAGCTTGCAGCAACGCCAACCTCAGGCGAGATGAGAGCAATCA
CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGG
10 CTACGTGCAGAGTCCTAGATTCCGAACAGCTACCCAGGAACCTGCTCCTG
ACATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTGACA
ATCAGTTGGATTAGAGGAAGCAGAAAATGATATCTGTAGGTATGATTGAT
GGAAGTTGAAGATATATCCGAAACCAGTACCAATTAGAGGACGATGGTGT
GGACACAAGGAAGTCCCTCCAAGGATAAAATCAAGAACGAACCAAATTAAA
15 ATCACATTCAAGTCCGATGACTACTTGTGGCTAACCTGGATTCAAGATTAA
TTATTCTTGCTGGAAGATTCCAACCCGAGCAGCTTCAGAGACCAACTGGG
AATCTGTCACAAGCTCTATTCAAGGGTATCCTATAACTCTCCATCAGAACG
GATCCCACTCTGATTGCGATGCTCTGGACAAAAAAATTGAGAATTGATA
CAGTGGAAAGATCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAAGATCT
20 TGAGAATATGTATCTGGACACCCCTCGGTATCGAGGCAGGTACACCATGAC
CGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAACGTTACA
GTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGC
CAATGTGGTCTTCTTCCACGTTGCCTCGTGCAGCGCTGTGGAGGAAATT
GTGGCTGTGGAACTGTCAACTGGAGGTCTGCACATGCAATTCAAGGAAAC
25 CGTAAAAAAAGTATCATGAGGTATTACAGTTGAGCCTGGCCACATCAAGAGG
AGGGTAGAGCTAACGACCATGGCTCTAGTGACATCCAGTTGGATCACCAG
AACGATGTGATTGTATCTGCAGCTCAAGACCACTCGATAAGAGAATGTGCA
CATCCTTACATTAAGCCTGAAAGAACCTTACGTTAAGGAGGGTGAGATAAG
AGACCCCTTCTACCAGCAACCAACTTACTACTAGCCTGCAATGCAATGAA
30 CACAAGTGGTTGCTGAGTCTCAGCCTTGCTTGTAAATGCCATGGCAAGTAGA
AAGGTATATCATCAACTTCTATACCTAACGAAATATAGGATTGCATTAAATAATA

GTGTTGAGGTATATGCACAAACACACACAGAAATATTGATGTCTATG
TGTATATAGATCAAATGTTTTGGTATATATAACCAGGTACACCAGAGCT
TACATATGTTGAGTTAGACTCTTAAACCTTGCCTAAAGGGATGGTC
AAATATGAAACATGTCTTAGAAAATTAGGAGATAAAATTATTTAAAT
5 TTTGAAACACAAAACAATTGAAATCTGCTCTTAAAGAAAGCATCTTGTAA
TATTAAAAATCAAAAGATGAGGCTTACATACATCTTAGTTG (SEQ ID
NO:50)

FIGURE 2

1 CTAaaaaatATGTTCTCTACAACACCAAGGCTCATTAaaaATTT
46 TAAATATTAATATAcATTCTTCTGTcAGAAATACATAAAACTTT
5 91 ATTATATCAGCGCAGGGCGGCGCGCTCGGTCCCGGGAGCAGAA
136 CCCGGCTTTCTGGAGCGACGCTGTCTAGTCGCTGATCCCA

181 AATGCACCGGCTCATTTGTCTACACTCTAATCTGCGCAAACCTT
MetHisArgLeuIlePheValTyrThrLeuIleCysAlaAsnPhe
10 226 TTGCAGCTGTCGGACACTTCTGCAACCCCGCAGAGCGCATCCAT
CysSerCysArgAspThrSerAlaThrProGlnSerAlaSerIle

271 CAAAGCTTGCGCAACGCCAACCTCAGGCGAGATGAGAGCAATCA
LysAlaLeuArgAsnAlaAsnLeuArgArgAspGluSerAsnHis
15 316 CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGG
LeuThrAspLeuTyrArgArgAspGluThrIleGlnValLysGly

361 AAACGGCTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAG
AsnGlyTyrValGlnSerProArgPheProAsnSerTyrProArg
20 406 GAACCTGCTCCTGACATGGCGGTTCACTCTCAGGAGAATACACG
AsnLeuLeuLeuThrTrpArgLeuHisSerGlnGluAsnThrArg
25 451 GATACAGCTAGTGTGACAATCAGTTGGATTAGAGGAAGCAGA
IleGlnLeuValPheAspAsnGlnPheGlyLeuGluGluAlaGlu

496 AAATGATATCTGTAGGTATGATTTGTGGAAGTTGAAGATATAC
30 AsnAspIleCysArgTyrAspPheValGluValGluAspIleSer

541 CGAAACCAGTACCAATTATTAGAGGACGATGGTGTGGACACAAGGA
GluThrSerThrIleIleArgGlyArgTrpCysGlyHisLysGlu

586 AGTCCTCCAAGGATAAAATCAAGAACGAAACCAATTAAAATCAC
35 ValProProArgIleLysSerArgThrAsnGlnIleLysIleThr

631 ATTCAAGTCCGATGACTACTTGTGGCTAACCTGGATTCAAGAT
PheLysSerAspAspTyrPheValAlaLysProGlyPheLysIle
40 676 TTATTATTCTTGCTGGAAGATTCCAACCCGCAGCAGCTTCAGA
TyrTyrSerLeuLeuGluAspPheGlnProAlaAlaAlaSerGlu

721 GACCAACTGGGAATCTGTCACAAGCTCTTTCAAGGGGTATCTA
 ThrAsnTrpGluSerValThrSerSerIleSerGlyValSerTyr

 5 766 TAACTCTCCATCAGTAACGGATCCCCTGATTGCGGATGCTCT
 AsnSerProSerValThrAspProThrLeuIleAlaAspAlaLeu

 811 GGACAAAAAAATTGCAGAATTGATACTGGAAAGATCTGCTCAA
 AspLysLysIleAlaGluPheAspThrValGluAspLeuLeuLys

 10 856 GTACTTCAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTA
 TyrPheAsnProGluSerTrpGlnGluAspLeuGluAsnMetTyr

 15 901 TCTGGACACCCCTCGGTATCGAGGCAGGTCATACCAGGAA
 LeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLys

 946 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTA
 SerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyr

 20 991 CAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCT
 SerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu

 1036 GAAGTTGCCAATGTGGCTCTTCCACGTTGCCTCCTCGTGCA
 LysLeuAlaAsnValValPhePheProArgCysLeuLeuValGln

 25 1081 GCGCTGTGGAGGAAATTGTGGCTGTGGAAGTGTCAACTGGAGGTC
 ArgCysGlyGlyAsnCysGlyCysGlyThrValAsnTrpArgSer

 1126 CTGCACATGCAATTCAAGGGAAAACCGTGAAAAAGTATCATGAGGT
 CysThrCysAsnSerGlyLysThrValLysLysTyrHisGluVal

 1171 ATTACAGTTGAGCCTGGCACATCAAGAGGGAGGGTAGAGCTAA
 LeuGlnPheGluProGlyHisIleLysArgArgGlyArgAlaLys

 35 1216 GACCAGGGCTCTAGTTGACATCCAGTTGGATCACCAGAACGATG
 ThrMetAlaLeuValAspIleGlnLeuAspHisHisGluArgCys

 1261 TGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGTGCA
 AspCysIleCysSerSerArgProProArg (SEQ ID NO:12)

 40 1306 CATCCTTACATTAAGCCTGAAAGAACCTTAGTTAAGGAGGGTG
 1351 AGATAAGAGACCCTTTCTACCAGCAACCAAACCTACTACTAGC
 1396 CTGCAATGCAATGAACACACAAGTGGTGCTGAGTCTCAGCCTTGCT

1441 TTGTTAATGCCATGGCAAGTAGAAAGGTATATCATCAACTCTAT
1486 ACCTAAGAATATAGGATTGCATTAATAATAGTGGTTGAGGTTAT
1531 ATATGCACAAACACACAGAAATATATTCTATGTCTATGTGTATA
1576 TAGATCAAATGTTTTGGTATATATAACCAGGTACACCAGAG
5 1621 CTTACATATGTTGAGTTAGACTCTAAAATCCTTGCCAAATA
1666 AGGGATGGTCAAATATATGAAACATGTCCTTAGAAAATTAGGAG
1711 ATAAATTATTTAAATTGAAACACAAAACAATTGAAATCT
1756 TGCTCTCTTAAAGAAAGCATCTGTATATTAAAAATCAAAAGATG
1801 AGGCTTCATACATACATCTTAGTTG (SEQ ID NO:50)

10

FIGURE 3

A -- Cur2 1.6 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGATTCAACTTCAGAACCTATAACATGAAC
TGGGTCCGCCAGGCTCCAGGGAAAGGGCTGGAGTGGGTCTCATCCATTAGTA
GTAGTAGTAGTAACATATACTACGCAGACTCAGTGAAGGGCCGATTACCAT
10 CTCCAGAGACAAAGCCAAGAACACTCACTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTATATTACTGTGCGAGAGATATTATGATTACGTTG
GGGAAATTATCGCCTCGTTCTACTTGACTACTGGGGCCAGGGAACCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:55)

B -- Cur2 1.6 heavy chain amino acid sequence

15 EVQLVESGGGLVKPGGSLRLSCAASGFNFRTYNMNWVRQAPGKGLEWVSSISSSS
SSNIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDIMITFGGIAS
FYFDYWGQGTLTVSS (SEQ ID NO:13)

20 C -- Cur2 1.6 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
25 TTTCAGCAGAAACCAGGGAAAGCCCTAAGCCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGCTCACTTCGGCGAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:56)

30 D -- Cur2 1.6 light chain amino acid sequence

DIQMTQSPSSLASVGDRVTITCRASQGIRNDLGWFQQKPGKAPKRLIYASSLQ
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGTKVEIK (SEQ
ID NO:14)

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FIGURE 4

A -- Cur2 1.11 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCTGGAGGAGGCTTGATCCAGCCTGGGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGGTCACCGTCAGTAGCAACTACATGAGC
TGGGTCCGCCAGGCTCAGGGAAGGGGCTGGAGTGGGTCTCAGTTATTATA
GCGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTC
CAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCC
10 GAGGACACGGCCGTGTATTACTGTGCGGGAACGGTGAACGAACTACGAATTACTACT
ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG (SEQ
ID NO:57)

B -- Cur2 1.11 heavy chain amino acid sequence

15 EVQLVQSGGLIQPGGLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSG
GSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGTVTTNYYGM
DVWGQGTTVTVSS (SEQ ID NO:15)

C -- Cur2 1.11 light chain nucleotide sequence

20 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCTGCAAAGTAATGGATAC
AACTATTGGATTGGTACCTGCAGAACGCCAGGGCAGTCTCCACAGCTCCTGA
TCTATTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCACTGGCAGT
GGATCAGGCACAGATTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATG
25 TTGGGGTTTATTACTGCATGCAAGCTACAAACTCTCACTTCGGCGGAGGG
ACCAAGGTGGAGATCAAAC (SEQ ID NO:58)

D -- Cur2 1.11 light chain amino acid sequence

30 DIVMTQSPLSLPVTPGEPASISCRSSQSLLQSNGNYLDWYLQKPGQSPQLIYLG
SNRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLFGGGTKVEI
K (SEQ ID NO:16)

FIGURE 5

A -- Cur2 1.17 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCCTGGTCCAGCCTGGGAAGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGCAGTTATGGT
ATGATGGAAGTAATAAACTATGCAGACTCCGTGAAGGGCCGATTACCAT
10 CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTATTACTGTGCGAGAGATCAAGGATACAGATATG
CTGGTTACTACTACGACTACGGTATGGACGTCTGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:59)

15 B -- Cur2 1.17 heavy chain protein sequence

QVQLVESGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIW
YDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYRYA
20 GYYDYGMDVWGQGTTVTVSS (SEQ ID NO:17)

25 C -- Cur2 1.17 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
25 GTTGCAAAGTGGGTCCCATCAAGGTTAGCGGGCAGTGGATCTGGGACAGA
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTCGAACCTTAACT
GTCTACAGCATAATAGTTACCCGCTCACITTCGGCGGAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:60)

30 D -- Cur2 1.17 light chain protein sequence

DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGTKVEIK (SEQ
35 ID NO:18)

FIGURE 6

A -- Cur2 1.18 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTCTGGATACACCTCACCGATTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA
CCCAAACAGTGGTAACACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC
10 ATGACCAGGAACACCTCCATAAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAGGGTATAGCAGTGGC
TGGGACATACTACTACTACGGTATGGACGTCTGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:61)

15 B -- Cur2 1.18 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAG
20 TYYYYYGMVDWGQGTTVTVSS (SEQ D NO:19)

25 C -- Cur2 1.18 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCTGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGAAACCAGGGAAAGGCCCTAACGCGCCTGATCTATGCTGCATCCA
25 GTTGCAAAGTGGGGTCCCATTCAAGGTTCAGCGGCAGTGGATCTGGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTCGAACTTATTCT
GTCTACAGCATAATAGTTACCCATTCACTTCCGGCCCTGGGACCAAAGTGGAT
ATCAAAC (SEQ ID NO:62)

30 D -- Cur2 1.18 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYFCLQHNSYPFTFGPGTKVDIK (SEQ
35 ID NO:20)

FIGURE 7

A -- Cur2 1.19 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCTGGGCTGAGGTGAAGAAGCCTGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTCTGGATACACCTCACCAAGTTATGATATCAAC
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAAC
CCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACCA
10 TGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG
ATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACGTTATGATTACGTTG
GGGGAGTTATCGTGCACTACGGTATGGACGTCTGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:63)

B -- Cur2 1.19 heavy chain amino acid sequence

15 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFG
GVIVHYGMDVWGQGTTVTVSS (SEQ ID NO:21)

20 C -- Cur2 1.19 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCCTCAAGGTTCAGCGGCAGTGGATCTGGGACAGA
TTTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTCACAATTACT
GTCTACAGCATAATAGTGAACCGTGCAGTTTGGCCAGGGACCAAGCTGGA
GATCAGAC (SEQ ID NO:64)

30 D -- Cur2 1.19 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYASSLQ
SGVPSRSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFQGKLEIR (SEQ
ID NO:22)

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FIGURE 8

A -- Cur2 1.23 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGAGTCT
CTGAAGATCTCCTGTGAGGGTCTGGATACAGCTTACCGACTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT
CCTGGTACTCTGATACCAGATACAGCCGTCCTCCAAGGCCAGGTACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
10 GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGTATCGTATTACTATG
TTTCGGGGAGTTATTATAACGTCTTGACTACTGGGCCAGGGAACCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:65)

B -- Cur2 1.23 heavy chain amino acid sequence

15 EVQLVQSGAEVKKPGEISLKIISCEGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG
DSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHVSYYYVSGS
YYNVFDYWGQGTLTVSS (SEQ ID NO:23)

C -- Cur2 1.23 light chain nucleotide sequence

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGATACCAGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCACAGTGGGTCCCATCAAGGTTCAAGGGCAGCAGCCTGAAGATTGCAACTTATTACT
25 ATTCACTCTACAATCAGCACGCTGCAGCCTGAAGATTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:66)

D -- Cur2 1.23 light chain amino acid sequence

30 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQIPGKAPKRLIYAASSLQR
GVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFQGQTKVEIK (SEQ
ID NO:24)

FIGURE 9

A -- Cur2 1.24.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTCACTAGTTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGGAGATATGGT
ATGATGGAAGTAATAAACTATGCAGACTCCGTGAAGGGCCGATTACCAT
10 CTCCAGAGACAAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTATTATTGTGCAGAGAGATCAGGGATACAGCTATG
GTTACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCCTCTCCTCAG (SEQ ID NO:67)

15 B -- Cur2 1.24.1 heavy chain protein sequence

QVQLVESGGVVQPGRSRLSCAASGFSFSSYGMHWVRQAPGKGLEWVADIW
YDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYSYG
YVYYDYGMDVWGQGTTVTVSS (SEQ ID NO:25)

20 C -- Cur2 1.24.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
25 TATCAGCAGAAACCAGGGAAAGCCCCCTAACGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGTCCCATCAAGGTTCAAGGTCAGCGGCAGTGGATCTGGGACAGA
GTTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTCGAACCTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTGGCCAAGGGACCAAGGGTGG
AATCAAAC (SEQ ID NO:68)

30 D -- Cur2 1.24.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYASSLQ
SGVPSRSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
35 ID NO:26)

FIGURE 10

A -- Cur2 1.25.1 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCTGTAAGGGTCTGGATACAGGTTACCAAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT
CCTGGTGACTCTGATACCAAGATACAGCCGTCTTCCAAGGCCAGGTACCA
10 TCTCAGCCGACAAGTCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCAGACATGGATCGTATTATTATG
GTTCGGAGACTTATTATAATGTCTITGACTACTGGGCCAGGAAACCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:69)

B -- Cur2 1.25.1 heavy chain protein sequence

15 EVQLVQSGAEVKKPGESLKISCKSGYRFTSYWIGWVRQMPGKGLEWMGIIYPG
DSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYCARHGSYYGSET
YYNVFDYWGQGTLTVSS (SEQ ID NO:27)

20 C -- Cur2 1.25.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCACATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAACGGCTGATCTATGCTGCATCCA
25 GTTGCAAAGTGGGTCCCATCAAGGTTCAAGGGCAGTGGATCTGGACAGA
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:70)

30 D -- Cur2 1.25.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFQGTKVEIK (SEQ
ID NO:28)

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FIGURE 11

A -- Cur2 1.29 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCGGGAGTCT
CTGAAGATCTCCTGTAAGGTTCTGGATACAGCTTACAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGATCATCTAT
CCTGGTGACTCTGATACCAAGATACAGCCCCTCCTCCAAGGCCAGGCCACCA
10 TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACGTGGATGTAGGGCT
ACGATTGGGGATATTACTATTACTACCAACGGTATGGACGTCTGGGCAAG
GGACCACGGTCACCGTCTCCTCAG (SEQ ID NO:71)

B -- Cur2 1.29 heavy chain protein sequence

15 EVQLVQSGAEVKPGESLKISCKSGYSFTSYWIGWVRQMPGKGLEWMGIYPG
DSDTRYSPSFQGQATISADKSISTAYLQWSSLKASDTAMYCARHVDVGATIGG
YYYYYHGMDVWGQGTTVTVSS (SEQ ID NO:29)

20 C -- Cur2 1.29 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCC
25 GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTGCATAGTAATGGATACA
ACTATTGGATTGGTACCTGCAGAAAGCCAGGGCAGTCTCCACAACCTCTGATC
TATTGGGTCTAATCGGGCCTCCGGGTCCCTGACAGGTCAGTGGCAGTGG
ATCAGGCACAGATTACACTGAAAATCAGCAGAGTGGAGGCTGACGATGTT
GGGGTTTATTACTGCATGCAAGCTACAATCTCATGTGCAGTTGGCCA
GGGGACCAAGCTGGAGATCAAAC (SEQ ID NO:72)

30 D -- Cur2 1.29 light chain protein sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLDWYLQKPGQSPQLLIYLG
SNRASGVPDFRSGSGSTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTLK
EIK (SEQ ID NO:30)

35

FIGURE 12

A -- Cur2 1.33 heavy chain nucleotide sequence

5 CAGGTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTACCAAGCTATGGTATCAGC
TGGGTGCACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCG
CTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAGAGTCACCAT
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG
10 ATCTGACGACACGGCCGTATTACTGTGCAGAGATCATTACTATGATAGT
AGTGATTATCTCTACTACTACTACGGTTGGACGTCTGGGGCCAAGGGACCAC
GGTCACCGTCTCCTCAG (SEQ ID NO:73)

B -- Cur2 1.33 heavy chain protein sequence

15 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA
YNGNTNYAQKLQGRVTMTTDSTSTAYMELRSLRSDDTAVYYCARDHYYDSS
DYLYYYYGLDVWGQGTTVTVSS (SEQ ID NO:31)

20 C -- Cur2 1.33 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT
ATCAGCAGAAACCAGGGAAAGTCCTAAAGCTCCTGATCTATGCTGCATCCAC
TTTGCAATCAGGGTCCCCTCTGGTTCACTGGCAGTGGATCTGGGACAGATT
TCACTCTCACCCTCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGT
CAAAAGTATAACAGTGCCCGCTCACTTCGGCGAGGGACCAAGGTGGAGA
TCAAAC (SEQ ID NO:74)

30 D -- Cur2 1.33 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQ
SGVPSRFSGSQSGTDFLTISLQPEDVATYYCQKYNSAPLTFGGGTKVEIK (SEQ
ID NO:32)

35

FIGURE 13

A -- Cur2 1.38.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGGAGTCGGGGGAGGCCTGGTCCAGCCTGGAGGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGCAATTATATGGT
ATGATGGAATGATAAATACTATGCAGACTCCGTGAAGGGCCGCTTCACCGT
10 CTCCAGAGACAATTCCAAGAACACGCTGTATGCAAATGAACAGCCTGAGA
GCCGAGGGACACGGCTGTATTACTGTGCGAGAGGGATATTACTATGATAGTA
GTGATTATCTCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCAC
GGTCACCGTCTCCTCAG (SEQ ID NO:75)

B -- Cur2 1.38.1 heavy chain protein sequence

15 QVQLVESGGVVQPGRLSLSCAASGFTFSSYGMHWVRQAPGKGLEWVVAIIVY
DGNDKYYADSVKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCARGYYYDSS
DYLYYYYGMDVWGQGTTVTVSS (SEQ ID NO:33)

20 C -- Cur2 1.38.1 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGT
ATCAGCAGAAACCAGGGAAAGTTCTAACCTCCTGATCTATGCTGCATCCAC
TTGCAATCAGGGTCCCCTCGGTTAGTGGCAGTGGATCTGGACAGATT
TCTCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAGCTTATTACTGT
CAAAGTGTAAACAGTGCCCCGTGGACGTTGGCCAAGGGACCACGGTGGAG
ATCAAAC (SEQ ID NO:76)

30 D -- Cur2 1.38.1 light chain protein sequence

35 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPNLLIYAASTLQ
SGVPSRFSGSGSGTDFSLTISSLQPEDVAAYYCQKCNSAPWTFQGTTVEIK (SEQ
ID NO:34)

FIGURE 14

A -- Cur2 1.39.1 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGAACAGAGGTGAAAAAGCCGGGGAGTCT
 CTGAAGATCTCCTGTAAGGGTCTGGATACAGGTTTACCACTACTGGATCGG
 CTGGGTGCGCCAGATGCCCGGAAAGGCCCTGGAGTGGATGGGATCATCTAT
 CCTGGTGA CTCGATACCAAGATACAGCCGTCCTCCAAGGCCAGGTACCA
 TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
10 GGCCTCGGACACCGCCATGTATTACTGTGCAGACATGGATCGTATTACTATA
 ATTGGGGAGTTATTATAACGTCTTGACTACTGGGCCAGGGAACCTGGTC
 ACCGTCTCCTCAG (SEQ ID NO:77)

B -- Cur2 1.39.1 heavy chain protein sequence

15 EVQLVQSGTEVKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPG
 DSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSYYNSGS
 YYNVFDYWGQGTLVTVSS (SEQ ID NO:35)

20 C -- Cur2 1.39.1 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
 AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
 TATCAGCAGAAACCAGGGAAAGCCCCTAACGCCTGATCTATGCTGCATCCA
 GTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGACAGA
 ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT
 GTCTACAGCATAATAGTTACCCGTGGACGTTGGCCAAGGGACCAAGGTGGA
 AATCAAAC (SEQ ID NO:78)

30 D -- Cur2 1.39.1 light chain protein sequence

35 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
 SGVPSRFSGSGSGTEFTLTSSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
 ID NO:36)

FIGURE 15

A -- Cur2 1.40.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTCTGGATAACACCTCACCACTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTGAGTGGATGGATGGATGAA
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC
10 ATGACCAGGAACACCTCCCTAACGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTATTACTGTGCGAGAGATATTGTAGTGGTGGT
AGCTGCTACCAACTACTACAACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:79)

B -- Cur2 1.40.1 heavy chain protein sequence

15 QVQLVQSGAEVKPGASVKVSCKASGYFTTYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSLSTAYMELSSLRSEDTAVYYCARDIVVVV
AATNYYNGMDVWGQGTTVTVSS (SEQ ID NO:37)

20

FIGURE 16

A -- Cur2 1.45 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTCTGGATAACACCTCACCAAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
10 CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
15 GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGCAGTGGATACAGCTA
TGGTTACGACTACTACTACGGTATGGACGTCTGGGCCAAGGGACCACGGTC
ACCGTCTCCTCAG (SEQ ID NO:80)

B -- Cur2 1.45 heavy chain protein sequence

15 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSYG
20 YDYYYYGMDVWGQGTTVTVSS (SEQ ID NO:38)

C -- Cur2 1.45 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCAATTGCCGGCGAGTCAGGGCATTAGCAATGATTAGCCTGG
TATCAGCAGAAACCAGGGAAAGTTCTAAGCTCCTGATCTATGCTGCATCCA
CTTGCAATTAGGGTCCCATCTGGTCAGTGGCAGTGGATCTGGACAGAT
30 TTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTG
TCAAAAGTATAAACAGTGCCTGACTTCAGTGGCCCTGGACCAAAGTGGAT
ATCAAAC (SEQ ID NO:81)

D -- Cur2 1.45 light chain protein sequence

35 DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAASTLQ
LGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNNSAPFTFGPGTKVDIK (SEQ
ID NO:39)

FIGURE 17

A -- Cur2 1.46.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTCTGGATACTCCTCACCAAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA
CCCTAACAAATGGTAACACAGGCTATGCACAGAACAGTTCCAGGGCAGAGTCACC
10 ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT
AACTGCTACGGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:82)

B -- Cur2 1.46.1 heavy chain protein sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYDINWVRQATGQGLEWMGWM
NPNNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVT
ATDYYYGMDVWGQGTTVTVSS (SEQ ID NO:40)

20 C -- Cur2 1.46.1 light chain nucleotide sequence

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAACGCCTGATTTGCTGCATCCA
GTTCGCCAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGA
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACT
GTCTACAGCATAGTGGTTACCCCTCCGACGTTGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:83)

30 D -- Cur2 1.46.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIFAASSLPS
GVPSRSGSGSGTEFTLTISLQPEDFATYYCLQHSGYPPTFGQGTKVEIK (SEQ ID
NO:41)

35

FIGURE 18

A -- Cur2 1.48.1 heavy chain nucleotide sequence

5 CAGGTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTACCAAGCTATGGTATCAGC
TGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCG
CTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAGAGTCACCAT
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG
10 ATCTGACGACACGGCCGTATTACTGTGCGAGAGATGTTGAATATTACTATG
ATGGTAGTGGTTATTACTACTTGAECTACTGGGGCCAGGGAACCCCTGGTCACC
GTCTCCTCAG (SEQ ID NO:84)

B -- Cur2 1.48.1 heavy chain protein sequence

15 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA
YNGNTNYAQKLQGRVTMTDTSTAYMELRSLSDDTAVYYCARDVEYYYD
GSGYYYFDYWGQGTLTVVSS (SEQ ID NO:42)

20 C -- Cur2 1.48.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCTTCCGTGTGCATCTGTAGGAGACAG
AGTCACCATCACTTGTGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGG
TATCAGCAGAAACCAGGGAAAGGCCCTAACGGTTCAAGGTTCAAGGTTCAAGG
25 TTTGCAAAGTGGGTCCCATTCAAGGTTCAAGGTTCAAGGTTCAAGGTTCAAGG
TTTCACTCTCACCATCAGCAGCCTGCAGCCTGAGGATTTCATCTTACTATT
GTCAACAGTCTAACAGTTCCCTCGGACGTTGGCCAAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:85)

30 D -- Cur2 1.48.1 light chain protein sequence

DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASILQ
SGVPSRFSGSGSGTDFTLTISLQPEDFASYYCQQSNSFPRTFGQGTKVEIK (SEQ
ID NO:43)

35

FIGURE 19

A -- Cur2 1.49.1 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTCTGGATAACACCTCACCAAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA
CCCTAACAGTGGTACACAGGGCTATGCACAGAACAGTTCCAGGGCAGAGTCACC
10 ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCGTGTATTCTGTGCGAGAACATGAGGGATATAGTGGC
TACGAGCTATTACTACTACCTACGGTATGGACGTCTGGGCCAAGGGACC
ACGGTCACCGTCTCCTCAG (SEQ ID NO:86)

B -- Cur2 1.49.1 heavy chain protein sequence

15 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGDTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCARMRDIVAT
SYYYYFYGMDVWGQGTTVTVSS (SEQ ID NO:44)

20 C -- Cur2 1.49.1 light chain nucleotide sequence

25 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA
ACTATTGGATTGGTACCTGCTGAAGCCAGGGCAGTCTCCACAGCTCCTGATC
TATTGGGTTCTAGTCGGGCCTCCGGGGTCCCTGACAGGTTAGTGGCAGTGG
ATCAGGCACAGATTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT
GGGGTTTATTACTGCATGCAAACCTACAAACTATCACCTCGGCCAAGGGAA
CACGACTGGAGATTAAAC (SEQ ID NO:87)

30 D -- Cur2 1.49.1 light chain protein sequence

35 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNLDWYLLKPGQSPQLLIYLG
SSRASGVPDFSGSGSTDFTLKISRVEADVGVYYCMQLQTLITFGQGTRLEIK
(SEQ ID NO:45)

FIGURE 20

A -- Cur2 1.51 heavy chain nucleotide sequence

5 GAGGTGCAGCTGGTGCAGTCGGGAGCTGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTCTGGATACAGCTTACCAAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT
CCTGGTGAECTGATGCCAAATACAGCCGTCTTCCAAGGCCAGGTACCA
10 TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCAGACACTATGATTACGTTGGA
GGAATTATCGGTATACAGGGTGGTCAACCCCTGGGCCAGGAACCTGGT
CACCGTCTCCTCAG (SEQ ID NO:88)

B -- Cur2 1.51.1 heavy chain protein sequence

15 EVQLVQSGAEVKPGESLKISCKSGYSFTSYWIGWVRQMPGKGLEWMGIIYPG
DSDAKYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYCARHYDYVWRNY
RYTGWFDPWGQGTLTVSS (SEQ ID NO:46)

20 C -- Cur2 1.51.1 light chain nucleotide sequence

25 GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTGTCTTGTCTCCAGGGGAAAG
AGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTAGCAGCAGCTACTTAGCC
TGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCAT
CCAACAGGGCCACTGGCATCCCAGACAGGTTAGTGGCAGTGGTCTGGGAC
AGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGAGTTGCAGTGTATT
ACTGTCAGCAGTATGGTAGCTCACTATTCACTTCCGGCCCTGGGACCAAAGTG
GATATCAAAC (SEQ ID NO:89)

30 D -- Cur2 1.51.1 light chain protein sequence

35 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRA
TGIPDRFSGSGSGTDFLTISRLEPEDFAVYYCQQYGSLSFTFGPGTKVDIK (SEQ
ID NO:47)

35

FIGURE 21

A -- Cur2 6.4 heavy chain nucleotide sequence

5 CAGGTGCAGCTGGTGCAGTCTGGGCTGAGGTGAAGAAGCCTGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTCTGGATACACCTCACCAAGTTATGATATCAAC
10 TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATAAAC
CTTAATAGTGGTAACACAGACTATGCACAGAACAGTTCCAGGGCAGAGTCACCA
TGACCAGGGACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG
ATCTGAGGACACGGCCATATATTATTGTGTGAGAGGCTTGGATACAGCTAT
15 AATTACGACTACTATTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCA
CCGTCTCCTCAGT (SEQ ID NO:90)

B -- Cur2 6.4 heavy chain amino acid sequence

15 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWIN
PNSGNTDYAQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNY
DYYYGMDVWGQGTTVTVSS (SEQ ID NO:48)

C -- Cur2 6.4 light chain nucleotide sequence

20 GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTGTCTCCAGGGGAAAG
AGCCACCCCTCTCCTGCAGGCCAGTCAGAGTGTAGTAGTTACTTAGCCT
GGTACCAGCAGAACGCTGGCCAGGCTCCAGGCTCCTCATCTATGCTACATC
CAGCAGGGCCACTGGCATCCACAGACAGGTTAGTGGCAGTGGGTCTGGGACA
GACTTCACTCTACCATCAGCAGACTGGAGCCTGAAGATTTCAGTGTATT
25 CTGTCAGCAGTATGGTAGTTACCGTGCAGTTGGCCAGGGACCAAGCTG
GAAATCAAGC (SEQ ID NO:91)

D -- Cur2 6.4 light chain amino acid sequence

30 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRA
TGIPDRFSGSGSGTDFLTISRLPEDFAVYYCQQYGSSPCSFQGTKLEIK (SEQ
ID NO:49)

FIGURE 22A

Clone	Germline genes used			No. of Nucleotide/ Amino acid changes						
				FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
CR2	V	D	J	V				D & J		
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0
	VK	mix								
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0
1.51.1	VH	5-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0

FIGURE 22B

Clone	Germline genes used			No. of Nucleotide/ Amino acid changes							
		V	D	J	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
CR2		V	D	J	V					D & J	
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	mix									
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0
1.51.1	VH	5-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0

FIGURE 23

Figure 23A

						Section 1
	(1) 1	10	20	30	40	51
CUR2-1.6.1_HC	(1) EVQLVESGGGLVKGGSRLSCAASGF	NFR	YNNM	WVRQAPGKGLEWVSSI		
VH3-21	(1) EVQLVESGGGLVKGGSRLSCAASGFT	FSS	YSMNN	WVRQAPGKGLEWVSSI		
Consensus	(1) EVQLVESGGGLVKGGSRLSCAASGF		F SY	MNWVRQAPGKGLEWVSSI		
						Section 2
	(52) 52	60	70	80	90	102
CUR2-1.6.1_HC	(52) SSSSSNIIYYADSVKGRFTI	SRDN	AKNSLYLQM	NSLRAEDTA	YVYCARDIMI	
VH3-21	(52) SSSSYIYYADSVKGRFTI	SRDN	AKNSLYLQM	NSLRAEDTA	YVYCAR	---
Consensus	(52) SSSSS IYYADSVKGRFTI	SRDN	AKNSLYLQM	NSLRAEDTA	YVYCAR	
						Section 3
	(103) 103	110	126			
CUR2-1.6.1_HC	(103) TFGGIIASFYFDYWGQGT	LTV	VSS			
VH3-21	(99) -----					
Consensus	(103)					

5

Figure 23B

						Section 1
	(1) 1	10	20	30	40	51
CUR2-1.6.1_LC	(1) DIQMTQSPSSLSASVGDRV	ITCRASQ	GIRNDLGW	WQQKPGKAPKR	LIYAA	
A30	(1) DIQMTQSPSSLSASVGDRV	ITCRASQ	GIRNDLGW	WQQKPGKAPKR	LIYAA	
Consensus	(1) DIQMTQSPSSLSASVGDRV	ITCRASQ	GIRNDLGW	WQQKPGKAPKR	LIYAA	
						Section 2
	(52) 52	60	70	80	90	102
CUR2-1.6.1_LC	(52) SSIQSGVPSRFSGSGSGT	EF	LT	TISS	LIQPEDFATYYCLQHNSY	PLTFGGGT
A30	(52) SSIQSGVPSRFSGSGSGT	EF	LT	TISS	LIQPEDFATYYCLQHNSY	-----
Consensus	(52) SSIQSGVPSRFSGSGSGT	EF	LT	TISS	LIQPEDFATYYCLQHNSY	
						Section 3
	(103) 103	107				
CUR2-1.6.1_LC	(103) KVEIK					
A30	(96) -----					
Consensus	(103)					

10

FIGURE 24

Figure 24A

	(1)	10	20	30	40	51	Section 1
Cur2-1.11.1_HC	(1)	EVQLVESGGGLIQPGLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI					
VH3-53	(1)	EVQLVESGGGLIQPGLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI					
Consensus	(1)	EVQLVESGGGLIQPGLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI					Section 2
	(2)	52	60	70	80	90	102
Cur2-1.11.1_HC	(2)	YSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGTVTTN					
VH3-53	(2)	YSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR---					
Consensus	(2)	YSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA					Section 3
	(103)	103	110	120			
Cur2-1.11.1_HC	(103)	YYYGMDVWGQGTTVTVSS					
VH3-53	(98)	-----					
Consensus	(103)						

5

Figure 24B

	(1)	10	20	30	40	51	Section 1
CUR2-1.11.1_LC	(1)	DIVMTQSPFLSPVTPGEFASISCRSSQSLLQSNGNYLDWYLQKPGQSPQL					
A19	(1)	DIVMTQSPFLSPVTPGEFASISCRSSQSLLHSNGNYLDWYLQKPGQSPQL					
Consensus	(1)	DIVMTQSPFLSPVTPGEFASISCRSSQSLL SNGNYLDWYLQKPGQSPQL					Section 2
	(2)	52	60	70	80	90	102
CUR2-1.11.1_LC	(2)	LIYLGSNRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTF					
A19	(2)	LIYLGSNRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP--					
Consensus	(2)	LIYLGSNRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP					Section 3
	(103)	103	111				
CUR2-1.11.1_LC	(103)	GGGTKVEIK					
A19	(101)	-----					
Consensus	(103)						

FIGURE 25

Figure 25A

											Section 1
CR2-1.17.1 HC	(1) 1	10	20	30	40	50					
VH3-33	(1) QVQLVE8GGGVVQPGKSLRLSCAASGFTFSSYGMHWRQAPGKGLEWVAI										
Consensus	(1) QVQLVE8GGGVVQPGKSLRLSCAASGFTFSSYGMHWRQAPGKGLEWVAI										
											Section 2
CR2-1.17.1 HC	(52) 52	60	70	80	90	100					
VH3-33	(52) WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGY										
Consensus	(52) WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR										
											Section 3
CR2-1.17.1 HC	(103) 103	110	120								
VH3-33	(103) RYAGYYYDYGMDVWGQGTTTVVSS										
Consensus	(103) (99) -----										

5

Figure 25B

											Section 1
CR2-1.17.1 LC	(1) 1	10	20	30	40	50					
A30	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKEPGKAPKRLIYAA										
Consensus	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKEPGKAPKRLIYAA										
											Section 2
CR2-1.17.1 LC	(53) 53	60	70	80	90	100					
A30	(53) SLOSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKV										
Consensus	(53) SLOSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYF										
											Section 3
CR2-1.17.1 LC	(105) 1007										
A30	(105) EIK										
Consensus	(105) (96) ---										

FIGURE 26

Figure 26A

											Section 1	
	(1)	1	10	20	30	40	50	60	70	80	90	104
CR2-1.18_HC	(1)	QVQLVQSGAEVKKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMN										
VH1-8	(1)	QVQLVQSGAEVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMN										
Consensus	(1)	QVQLVQSGAEVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMN										
											Section 2	
	(53)	53	60	70	80	90	100	105	110	115	120	104
CR2-1.18_HC	(53)	PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSILRSEDTAVYYCAREGIAVA										
VH1-8	(53)	PNSGNTGYAQRFQGRVTMTRNTSISTAYMELSSILRSEDTAVYYCAR-----										
Consensus	(53)	PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSILRSEDTAVYYCAR										
											Section 3	
	(105)	105	110	115	120	125	130	135	140	145	150	155
CR2-1.18_HC	(105)	GTYYYYYYGMDVWGQGTTTVSS										
VH1-8	(99)	-----										
Consensus	(105)	-----										

5

Figure 26B

											Section 1	
	(1)	1	10	20	30	40	50	60	70	80	90	106
CR2-1.18_LC	(1)	DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS										
A30	(1)	DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS										
Consensus	(1)	DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS										
											Section 2	
	(54)	54	60	70	80	90	100	105	110	115	120	106
CR2-1.18_LC	(54)	LQSGVPSRFSGSGSGTEFTLTISISSLQPEDFATYFCLQHNSYPFTFGPGTKVDI										
A30	(54)	LQSGVPSRFSGSGSGTEFTLTISISSLQPEDFATYFCLQHNSYP-----										
Consensus	(54)	LQSGVPSRFSGSGSGTEFTLTISISSLQPEDFATYFCLQHNSYP										
											Section 3	
	(107)	107	110	115	120	125	130	135	140	145	150	155
CR2-1.18_LC	(107)	K										
A30	(96)	-										
Consensus	(107)	-----										

10

FIGURE 27

Figure 27A

	(1)	10	20	30	40	52	Section 1	
Cur2-1 19.1_hc	(1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN							
VH1-8	(1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN							
Consensus	(1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN							
	(53)	53	60	70	80	90	104	Section 2
Cur2-1.19.1_hc	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITE							
VH1-8	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR-----							
Consensus	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR							
	(105)	105	110	126				Section 3
Cur2-1 19.1_hc	(105) GGVIVHYGMDVVGQGTTTVVSS							
VH1-8	(99) -----							
Consensus	(105)							

5

Figure 27B

	(1)	10	20	30	40	52	Section 1	
Cur2-1 19.1_lc	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA							
A30	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA							
Consensus	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA							
	(53)	53	60	70	80	90	104	Section 2
Cur2-1.19.1_lc	(53) SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSPFGQGPKI							
A30	(53) SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSYP-----							
Consensus	(53) SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNS P							
	(105)	1087						Section 3
Cur2-1 19.1_lc	(105) EIR							
A30	(96) ---							
Consensus	(105)							

10

FIGURE 28

Figure 28A

						Section 1
	(1) 1	10	20	30	40	51
Cur2-1.23.1 HC	(1) EVQLVQSGAEVKKPGE SLK ^I 3CEGSGY S ^F TSYWI G ^W VRQMPGK G ^L EW M ^G II					
VH5-51	(1) EVQLVQSGAEVKKPGE SLK ^I 3CKGSGY S ^F TSYWI G ^W VRQMPGK G ^L EW M ^G II					
Consensus	(1) EVQLVQSGAEVKKPGE SLK ^I 3C GSGY S ^F TSYWI G ^W VRQMPGK G ^L EW M ^G II					
						Section 2
	(2) 52	60	70	80	90	102
Cur2-1.23.1 HC	(2) YPGDSDTRYSPSFQGQVTI S ^I ADKSISTAYLQW S ^I KA S ^D TAMYYCARHVSY					
VH5-51	(2) YPGDSDTRYSPSFQGQVTI S ^I ADKSISTAYLQW S ^I KA S ^D TAMYYCAR-----					
Consensus	(2) YPGDSDTRYSPSFQGQVTI S ^I ADKSISTAYLQW S ^I KA S ^D TAMYYCAR					
						Section 3
	(103) 103	110	126			
Cur2-1.23.1 HC	(103) YYVSGSYYNVFDYWGQGTLVTVSS					
VH5-51	(99) -----					
Consensus	(103)					

5

Figure 28B

						Section 1
	(1) 1	10	20	30	40	51
Cur2-1.23.1 LC	(1) DIQMTQSP SS ^I LSASVGDRVTITCRASQGIRNDLGWYQQIPGKAPKR L IYAA					
A30	(1) DIQMTQSP SS ^I LSASVGDRVTITCRASQGIRNDLGWYQQ K PGKAPKR L IYAA					
Consensus	(1) DIQMTQSP SS ^I LSASVGDRVTITCRASQGIRNDLGWYQQ PGKAPKR L IYAA					
						Section 2
	(2) 52	60	70	80	90	102
Cur2-1.23.1 LC	(2) SSLQRGVPSRFSGSGSGTEFTLT I SS L QPEDFATYYCLQHNSYPWTFGQGT					
A30	(2) SSLQSGVPSRFSGSGSGTEFTLT I SS L QPEDFATYYCLQHNSYP-----					
Consensus	(2) SSLQ GVPSRFSGSGSGTEFTLT I SS L QPEDFATYYCLQHNSYP					
						Section 3
	(103) 103 107					
Cur2-1.23.1 LC	(103) KVEIK					
A30	(96) -----					
Consensus	(103)					

10

FIGURE 29

Figure 29A

	(1)	10	20	30	40	51	Section 1
CR2-1.24.1_HC	(1) QVQLVESGGGVVQPGRSRLSCAASGFSFS						
VH3-33	(1) QVQLVESGGGVVQPGRSRLSCAASGFFSSYGMHWVRQAPGKGLENVADI						
Consensus	(1) QVQLVESGGGVVQPGRSRLSCAASGFSFS						
	(52)	60	70	80	90	102	Section 2
CR2-1.24.1_HC	(52) WYDGSNKYYADSVKGRFTI	SRDN	SKNTLYLQMN	SLRAEDTA	VYYCAR	QGY	
VH3-33	(52) WYDGSNKYYADSVKGRFTI	SRDN	SKNTLYLQMN	SLRAEDTA	VYYCAR	---	
Consensus	(52) WYDGSNKYYADSVKGRFTI	SRDN	SKNTLYLQMN	SLRAEDTA	VYYCAR		
	(103)	103	110	126			Section 3
CR2-1.24.1_HC	(103) SYGYVYYDYGMDVWGQGTTVTVSS						
VH3-33	(99) -----						
Consensus	(103)						

5

Figure 29B

	(1)	10	20	30	40	52	Section 1
CR2-1.24.1_LC	(1) DIQMTQSPSSLSASVGDRV	TITCRASQGIRNDLGWYQQKPGKAPKRLIYAA	S				
A30	(1) DIQMTQSPSSLSASVGDRV	TITCRASQGIRNDLGWYQQKPGKAPKRLIYAA	S				
Consensus	(1) DIQMTQSPSSLSASVGDRV	TITCRASQGIRNDLGWYQQKPGKAPKRLIYAA	S				
	(53)	53	60	70	80	90	104
CR2-1.24.1_LC	(53) SIQSGVPSRFSGSGSGCTEFTLT	TISSLQPEDFATYYCLQHNSYPWTFGQGTV					
A30	(53) SIQSGVPSRFSGSGSGCTEFTLT	TISSLQPEDFATYYCLQHNSYP-----					
Consensus	(53) SIQSGVPSRFSGSGSGCTEFTLT	TISSLQPEDFATYYCLQHNSYP					
	(105)	1067					Section 3
CR2-1.24.1_LC	(105) EIK						
A30	(96) ---						
Consensus	(105)						

10

FIGURE 30

Figure 30A

	(1)	10	20	30	40	51	Section 1
VH5-51	(1) EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII						
CR2-1.25.1_HC	(1) EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGII						
Consensus	(1) EVQLVQSGAEVKKPGESLKISCKGSGY FTSYWIGWVRQMPGKGLEWMGII						
	(2)	52	60	70	80	90	102
VH5-51	(2) YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR---						
CR2-1.25.1_HC	(2) YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHG8Y						
Consensus	(2) YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR						
	(103)	103	110	126			Section 3
VH5-51	(99) ---						
CR2-1.25.1_HC	(103) YYGSETYYNVFDYWGQGTLTVSS						
Consensus	(103)						

5

Figure 30B

	(1)	10	20	30	40	52	Section 1
A30	(1) DIQMTQSPSSLSASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS						
CR2-1.25.1_LC	(1) DIQMTQSPSSLSASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS						
Consensus	(1) DIQMTQSPSSLSASVGDRVITITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS						
	(53)	53	60	70	80	90	104
A30	(53) SLQSGVP SRF SGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP---						
CR2-1.25.1_LC	(53) SLQSGVP SRF SGSGSGTEFTLTISSLQPEDFATYYCLQHNSYFWTFGQGTV						
Consensus	(53) SLQSGVP SRF SGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP						
	(105)	1067					Section 3
A30	(96) ---						
CR2-1.25.1_LC	(105) EIK						
Consensus	(105)						

10

FIGURE 31

Figure 31A

	Section 1									
	(1) 1	10	20	30	40	50	52			
VH5-51	(1) EVQLVQSGAEVKKPGE	SLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYY								
CR2-1.29_HC	(1) EVQLVQSGAEVKKPGE	SLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYY								
Consensus	(1) EVQLVQSGAEVKKPGE	SLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYY								
	Section 2									
	(53) 53	60	70	80	90	100	104			
VH5-51	(53) PGDSDTTRYSESFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR	-----								
CR2-1.29_HC	(53) PGDSDTTRYSPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCAR	HVDVGA								
Consensus	(53) PGDSDTTRYSPSFQGQ	TISADKSISTAYLQWSSLKASDTAMYYCAR								
	Section 3									
	(105) 105	110	120	129						
VH5-51	(99) -----									
CR2-1.29_HC	(105) TIGGYYYYYHGMDVWGQGTTTVSS									
Consensus	(105)									

5

Figure 31B

	Section 1									
	(1) 1	10	20	30	40	50	53			
A19	(1) DIVMTQSPSLPVTGEPASISCRSSQSLLHSNGNYLDWYLQKPGQSPQLLI									
CR2-1.29_LC	(1) DIVMTQSPSLPVTGEPASISCRSSQSLLHSNGNYLDWYLQKPGQSPQLLI									
Consensus	(1) DIVMTQSPSLPVTGEPASISCRSSQSLLHSNGNYLDWYLQKPGQSPQLLI									
	Section 2									
	(54) 54	60	70	80	90	100	106			
A19	(54) YLGSNRASGVDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQP	-----								
CR2-1.29_LC	(54) YLGSNRASGVDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQELMCSFGQ									
Consensus	(54) YLGSNRASGVDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQS									
	Section 3									
	(107) 107	113								
A19	(101) -----									
CR2-1.29_LC	(107) GTKLEIK									
Consensus	(107)									

10

FIGURE 32

Figure 32A

						Section 1
VH1-18	(1)	10	20	30	40	52
CR2-1.33_HC	(1)	QVQLVQSGAEVKKPGASVKVSKASGTYFTSYG18WVRQAPGQGLEWMGWI8				
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSKASGTYFTSYG18WVRQAPGQGLEWMGWI8				
						Section 2
VH1-18	(53)	53	60	70	80	104
CR2-1.33_HC	(53)	AYNGNTNYAQKLQGRVTMTTDSTSTSTAYMELRSLRSDDTAVYYCAR-----				
Consensus	(53)	AYNGNTNYAQKLQGRVTMTTDSTSTSTAYMELRSLRSDDTAVYYCAR				
						Section 3
VH1-18	(105)	105	110	127		
CR2-1.33_HC	(105)	SDYLYYYYGLDVWGQGTTVTVSS				
Consensus	(105)					

5

Figure 32B

		Section 1				
CR2-1.33_LC	(1) <u>1</u>	10	20	30	40	53
	A20	(1) DIQMTQSPSSISASVGDRVITCRASQGISNYLAWYQQKPGKVPKLLIYAAST				
	Consensus	(1) DIQMTQSPSSISASVGDRVITCRASQGISNYLAWYQQKPGKVPKLLIYAAST				
Section 2						
CR2-1.33_LC	(54) <u>54</u>	60	70	80	90	106
	A20	(54) IQLSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAP-----				
	Consensus	(54) IQLSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPLTFGGGTKVEI				
Section 3						
CR2-1.33_LC	(107) <u>107</u>					
	A20	(96) -				
	Consensus	(107) K				

10

FIGURE 33

Figure 33A

	(1)	10	20	30	40	51	Section 1
VH3-33	(1) QVQLVESGGGVVQPGRSLRL	SCAASGFTF	S	SYGMHWVRQAPGKGLEWVAVI			
CR2-1.38.1_HC	(1) QVQLVESGGGVVQPGRSLRL	SCAASGFTF	S	SYGMHWVRQAPGKGLEWVAVI			
Consensus	(1) QVQLVESGGGVVQPGRSLRL	SCAASGFTF	S	SYGMHWVRQAPGKGLEWVAVI			
	(52)	60	70	80	90	102	Section 2
VH3-33	(52) WYDGSNKYYADSVKGRFTI	SRDNSKNTLYLQMNSLRAEDTAVYYCAR	---				
CR2-1.38.1_HC	(52) WYDGNDKYYADSVKGRFTI	SRDNSKNTLYLQMNSLRAEDTAVYYCAR	---				
Consensus	(52) WYDG	KYYADSVKGRFTI	SRDNSKNTLYLQMNSLRAEDTAVYYCAR				
	(103)	103	110	127			Section 3
VH3-33	(99) -----						
CR2-1.38.1_HC	(103) DSSDYLYYYYGMDVWGQGT	T	V	T	V	S	
Consensus	(103)						

5

Figure 33B

	(1)	10	20	30	40	52	Section 1
A20	(1) DIQMTQSPSSLSASVGDRV	TITCRASQG	I	SYLAWYQQKPGKVP	KLLIYAA	S	
CR2-1.38.1_LC	(1) DIQMTQSPSSLSASVGDRV	TITCRASQG	I	SYLAWYQQKPGKVP	NLLIYAA	S	
Consensus	(1) DIQMTQSPSSLSASVGDRV	TITCRASQG	I	SYLAWYQQKPGKVP	LLIYAA	S	
	(53)	60	70	80	90	104	Section 2
A20	(53) TLQSGVP	SRESGSGSGTDF	SLTISSLOPEDV	ATYYCQKYN	SAP	-----	
CR2-1.38.1_LC	(53) TLQSGVP	SRFSGSGSGTDF	SLTISSLOPEDV	AAYYCQKCNSA	PWTFGQGTTV		
Consensus	(53) TLQSGVP	SRFSGSGSGTDF	SLTISSLOPEDV	YYCQK	NSAP		
	(105)	1087					Section 3
A20	(96) -----						
CR2-1.38.1_LC	(105) EIK						
Consensus	(105)						

10

FIGURE 34

Figure 34A

	(1)	10	20	30	40	51	Section 1
VH5-51	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSGFTSYWIGWVRQMPGKGLEWMGII					
CR2-1.39 1_HC	(1)	EVQLVQSGTEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGII					
Consensus	(1)	EVQLVQSG EVKKPGESLKISCKGSGY FTSYWIGWVRQMPGKGLEWMGII					
	(52)	60	70	80	90	102	Section 2
VH5-51	(52)	YPGDS DTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR---					
CR2-1.39 1_HC	(52)	YPGDS DTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSY					
Consensus	(52)	YPGDS DTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR					
	(103)	103	110	126			Section 3
VH5-51	(99)	---					
CR2-1.39 1_HC	(103)	YYNSGSYYNVFDYWGQGTLTVSS					
Consensus	(103)						

5

Figure 34B

	(1)	10	20	30	40	52	Section 1
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA					
CR2-1.39 1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA					
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA					
	(53)	60	70	80	90	104	Section 2
A30	(53)	SLQSGVP SRFSGSGSGTEFTLTISLQPEDPATYYCLQHNSYP-----					
CR2-1.39 1_LC	(53)	SLQSGVP SRFSGSGSGTEFTLTISLQPEDPATYYCLQHNSYFWTFGQGTV					
Consensus	(53)	SLQSGVP SRFSGSGSGTEFTLTISLQPEDPATYYCLQHNSYP					
	(105)	1087					Section 3
A30	(96)	---					
CR2-1.39 1_LC	(105)	EIK					
Consensus	(105)						

10

FIGURE 35

Figure 35A

						Section 1
VH1-8	(1) 1	10	20	30	40	52
CR2-1.45_HC	(1) QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN					
Consensus	(1) QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN					
						Section 2
VH1-8	(53) 53	60	70	80	90	104
CR2-1.45_HC	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSED TAVYYCAR-----					
Consensus	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSED TAVYYCAR-----					
						Section 3
VH1-8	(105) 105	110	125			
CR2-1.45_HC	(99) -----					
Consensus	(105) GYDYYYYGMDVWGQGTTVTVSS					

5

Figure 35B

		Section 1				
		10	20	30	40	53
CR2-1.45_LC	A20	(1) DIQMTQSPSSISASAVGDRVТИCRASQGISNYLAWYQQKPGKVPKLLIYAAST				
	Consensus	(1) DIQMTQSPSSISASAVGDRVТИ CRASQGISN LAMYQQKPGKVPKLLIYAAST				
						Section 2
		54	60	70	80	106
CR2-1.45_LC	A20	(54) LQSGVP SRF SGSGSGTDF TLTISI LQPED VATYYCQKYN SAP -----				
	Consensus	(54) LQ LGVP SRF SGSGSGTDF TLTISI LQPED VATYYCQKYN SAP FTFGPGTKV D				
						Section 3
		(107) 107				
		A20 (96) -				
		CR2-1.45_LC (107) K				
		Consensus (107)				

10

FIGURE 36

Figure 36A

	Section 1					
	(1) 1	10	20	30	40	51
VH1-8	(1) QVQLVQSGAEVKPGASVKVSCKASGY	FTSYDINWVRQATGQGLEWMGWM				
CR2-1.46.1_HC	(1) QVQLVQSGAEVKPGASVKVSCKASGY	FTSYDINWVRQATGQGLEWMGWM				
Consensus	(1) QVQLVQSGAEVKPGASVKVSCKASGY	SFTSYDINWVRQATGQGLEWMGWM				
	Section 2					
	(2) 52	60	70	80	90	102
VH1-8	(2) NPNSGNTGYAQKFQGRVTMTRNTS	I STAYMEISSLRSEDTAVYYCAR	---			
CR2-1.46.1_HC	(2) NPNNGNTGYAQKFQGRVTMTRNTS	I STAYMEISSLRSEDTAVYYCAR	DIVV			
Consensus	(2) NPN	GNTGYAQKFQGRVTMTRNTS	I STAYMEISSLRSEDTAVYYCAR			
	Section 3					
	(103) 103	110	126			
VH1-8	(99) ---					
CR2-1.46.1_HC	(103) VVTATDYYYGMDVWGQGTTVTVSS					
Consensus	(103)					

5

Figure 36B

	Section 1					
	(1) 1	10	20	30	40	52
A30	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKR	LIFAAAS				
CR2-1.46.1_LC	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKR	LIFAAAS				
Consensus	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKR	LIFAAAS				
	Section 2					
	(53) 53	60	70	80	90	104
A30	(53) SLOSGVP	SRFSGSGSGTEFTLTIS	SSLQPEDFATYYCLQHNSYP	-----		
CR2-1.46.1_LC	(53) SLP3GVP	SRFSGSGSGTEFTLTIS	SSLQPEDFATYYCLQHSGYPP	TFGQGTV		
Consensus	(53) SL	SGVPSRFSGSGSGTEFTLTIS	SSLQPEDFATYYCLQH	YP		
	Section 3					
	(105) 1087					
A30	(96) ---					
CR2-1.46.1_LC	(105) EIK					
Consensus	(105)					

10

FIGURE 37

Figure 37A

	(1)	10	20	30	40	51	Section 1
CR2-1.48.1_HC	(1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWI						
VH1-18	(1) QVQLVQSGAEVKEPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWI						
Consensus	(1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWI						
							Section 2
	(2)	52	60	70	80	90	102
CR2-1.48.1_HC	(2) SAYNGNTNYAQKLQGRVTMTDTSTSTAYMELRSLRSDDTAVYYCARDVEY						
VH1-18	(2) SAYNGNTNYAQKLQGRVTMTDTSTSTAYMELRSLRSDDTAVYYCAR---						
Consensus	(2) SAYNGNTNYAQKLQGRVTMTDTSTSTAYMELRSLRSDDTAVYYCAR						
							Section 3
	(103)	103	110	125			
CR2-1.48.1_HC	(103) YYDGSGYYYYFDYWGQGTIVTVSS						
VH1-18	(99) -----						
Consensus	(103)						

5

Figure 37B

	(1)	10	20	30	40	52	Section 1
CR2-1.48.1_LC	(1) DIQMTQSPSSVSASVGDRVITCRASQGISSWILAWYQQKPGKAPKLLIYAA						
L5	(1) DIQMTQSPSSVSASVGDRVITCRASQGISSWILAWYQQKPGKAPKLLIYAA						
Consensus	(1) DIQMTQSPSSVSASVGDRVITCRASQGISSWILAWYQQKPGKAPKLLIYAA						
							Section 2
	(53)	53	60	70	80	90	104
CR2-1.48.1_LC	(53) ILQSGVPSRFSGSGSGTDFLTISLQPEDFASYYCQQANSFPRTFGQGTKV						
L5	(53) ILQSGVPSRFSGSGSGTDFLTISLQPEDFASYYCQQANSFP-----						
Consensus	(53) ILQSGVPSRFSGSGSGTDFLTISLQPEDFASYYCQQANSFP						
							Section 3
	(105)	1067					
CR2-1.48.1_LC	(105) EIK						
L5	(96) ---						
Consensus	(105)						

10

FIGURE 38

Figure 38A

						Section 1
	(1) 1	10	20	30	40	51
CR2-1.49.1_HC	(1) QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWM					
VH1-8	(1) QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWM					
Consensus	(1) QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWM					
						Section 2
	(2) 52	60	70	80	90	102
CR2-1.49.1_HC	(2) NPNSGDTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCARMRDI					
VH1-8	(2) NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCAR---					
Consensus	(2) NPNSG TGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCAR					
						Section 3
	(103) 103	110	127			
CR2-1.49.1_HC	(103) VATSYYYYFYGMDVWGQGTTTVSS					
VH1-8	(99) -----					
Consensus	(103)					

5

Figure 38B

						Section 1
	(1) 1	10	20	30	40	52
CR2-1.49.1_LC	(1) DIVMTQSPSLPVTGEPASISCRSSQSLLHSNGNYLDWYLLKPGQSPQLL					
A19	(1) DIVMTQSPSLPVTGEPASISCRSSQSLLHSNGNYLDWYLLKPGQSPQLL					
Consensus	(1) DIVMTQSPSLPVTGEPASISCRSSQSLLHSNGNYLDWYLLKPGQSPQLL					
						Section 2
	(53) 53	60	70	80	90	104
CR2-1.49.1_LC	(53) IYLGSSRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYCMQTLQQTITFGQ					
A19	(53) IYLGSNRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP---					
Consensus	(53) IYLGSS RASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYCMQ LQT					
						Section 3
	(105) 105	111				
CR2-1.49.1_LC	(105) GTRLEIK					
A19	(101) -----					
Consensus	(105)					

10

FIGURE 39

Figure 39A

						Section 1
	(1) 1	10	20	30	40	51
CR2-1.51.1_HC	(1) EVQLVQSGAEVKKPGESLKI	SCKGSGYSFTSYWIGWVRQMPGKGLEWMGII				
VH5-51	(1) EVQLVQSGAEVKKPGESLKI	SCKGSGYSFTSYWIGWVRQMPGKGLEWMGII				
Consensus	(1) EVQLVQSGAEVKKPGESLKI	SCKGSGYSFTSYWIGWVRQMPGKGLEWMGII				
						Section 2
	(52) 52	60	70	80	90	102
CR2-1.51.1_HC	(52) YPGDSDAKYSESFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHYDY					
VH5-51	(52) YPGDSDT K YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR	---				
Consensus	(52) YPGDSD	KYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR				
						Section 3
	(103) 103	110	120	126		
CR2-1.51.1_HC	(103) VWRNYRYTGWFDPWGQGTLVTVSS					
VH5-51	(99) -----					
Consensus	(103)					

5

Figure 39B

						Section 1
	(1) 1	10	20	30	40	52
CR2-1.51.1_LC	(1) EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGA					
A27	(1) EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGA					
Consensus	(1) EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGA					
						Section 2
	(53) 53	60	70	80	90	104
CR2-1.51.1_LC	(53) S N RATGIPDRFSGSGSGTDF T LTISRL E PEDFAVYYCQQY G SSL F TF G PGTK					
A27	(53) S N RATGIPDRFSGSGSGTDF T LTISRL E PEDFAVYYCQQY G SSP	---				
Consensus	(53) S RATGIPDRFSGSGSGTDF T LTISRL E PEDFAVYYCQQY G SS					
						Section 3
	(105) 10508					
CR2-1.51.1_LC	(105) VDIK					
A27	(97) ---					
Consensus	(105)					

10

FIGURE 40

Figure 40A

	(1)	1	10	20	30	40	52	Section 1
Cur2-6.4.1_hc	(1)	QVQLVQSGAEVKPGASVKVSKAASGYTFTSYDINWVRQATGQGLEWMGN						
VH1-8	(1)	QVQLVQSGAEVKPGASVKVSKAASGYTFTSYDINWVRQATGQGLEWMGN						
Consensus	(1)	QVQLVQSGAEVKPGASVKVSKAASGYTFTSYDINWVRQATGQGLEWMGN						
	(53)	53	60	70	80	90	104	Section 2
Cur2-6.4.1_hc	(53)	PNSGNTDYAQKFQGRVTMTRDTSI	STAYMELSSLRSEDTA	YYCVR.GFGYSY				
VH1-8	(53)	PNSGNTGYAQKFQGRVTMTRN	TSI	STAYMELSSLRSEDTA	YYCAR			
Consensus	(53)	PNSGNT	YAQKFQGRVTMTR	TSI	STAYMELSSLRSEDTA	YYC R		
	(105)	105	110	125				Section 3
Cur2-6.4.1_hc	(105)	NYDYYYGMDVNGQGTTVTVSS						
VH1-8	(99)	-----						
Consensus	(105)							

5

Figure 40B

	(1)	1	10	20	30	40	52	Section 1
Cur2-6.4.1_Lc	(1)	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIY						
A27	(1)	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIY						
Consensus	(1)	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIY						
	(53)	53	60	70	80	90	104	Section 2
Cur2-6.4.1_Lc	(53)	SSRATGIPDRFSGSGSGTDFLTISRL	EEEDFAVYYCQQYGS	SPCSFGQG	TK			
A27	(53)	SSRATGIPDRFSGSGSGTDFLTISRL	EEEDFAVYYCQQYGS	SPCSFGQG	TK			
Consensus	(53)	SSRATGIPDRFSGSGSGTDFLTISRL	EEEDFAVYYCQQYGS	SPCSFGQG	TK			
	(105)	10908						Section 3
Cur2-6.4.1_Lc	(105)	LEIK						
A27	(97)	---						
Consensus	(105)							

10

FIGURE 41

Clone #	VH L	#DE	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH # del	JH Segment
1.19.1	DP-15/1-8	-1	CGAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B	-12 ACTACG (SEQ ID NO:94)
1.19.2	DP-15/1-8	-1	CGAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B	-12 ACTACG (SEQ ID NO:94)
1.19.3	DP-15/1-8	-1	CGAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B	-12 ACTACG (SEQ ID NO:94)
6.4.1	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGGATAACAGCTA (SEQ ID NO:96)	2	TA	JH6 B	0 ATTACTAC (SEQ ID NO:97)
6.4.2	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGGATAACAGCTA (SEQ ID NO:96)	2	TA	JH6 B	0 ATTACTAC (SEQ ID NO:97)
6.4.3	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGGATAACAGCTA (SEQ ID NO:96)	2	TA	JH6 B	0 ATTACTAC (SEQ ID NO:97)
Clone	vk	#de	vk end	#n	N SEQ	JK	# del	JK end				
1.19.1	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)				
1.19.2	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)				
1.19.3	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)				
6.4.1	A27/A27A	-3	CTCACCC (SEQ ID	6	GTGCAG (SEQ ID	JK2	-7	TTTTGG (SEQ ID				

6.4.2	A27/A27A	-3	NO:101)	NO:102)	JK2	-7	NO:103)
			CTCACCC (SEQ ID NO:101)	6 (SEQ ID NO:102)	GTGCAG (SEQ ID NO:102)		TTTTGG (SEQ ID NO:103)
6.4.3	A27/A27A	-3	NO:101)	NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)
			CTCACCC (SEQ ID NO:101)	6 (SEQ ID NO:102)	GTGCAG (SEQ ID NO:102)		

FIGURE 42

CLONE #	VH	#DEL	VH END N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH del	JH Segment
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	D3-16	22	TATTATGATTAC GTTTGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1 CTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	D3-16	22	TATTATGATTAC GTTTGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1 CTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	D3-16	22	TATTATGATTAC GTTTGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1 CTACTT (SEQ ID NO:107)
1.11.1	DP-42/3-53	-5	AGAGA (SEQ ID NO:108)	3	GGA	10	ACGGTGACTA (SEQ ID NO:105)	5	CGAAT (SEQ ID NO:106)	JH6B	-2 TACTACT (SEQ ID NO:107)
1.11.2	DP-42/3-53	-5	AGAGA (SEQ ID NO:108)	3	GGA	10	ACGGTGACTA (SEQ ID NO:109)	5	CGAAT (SEQ ID NO:110)	JH6B	-2 TACTACT (SEQ ID NO:111)
1.23.1	DP-73/5-51	0	GAGACA (SEQ ID NO:112)	18	TGTATCGTATTACT ATGT (SEQ ID NO:113)	19	TTCGGGGAGTTA TTATAAC (SEQ ID NO:114)	2	GT	JH4B	-4 CTTTGA (SEQ ID NO:115)
1.23.2	DP-73/5-51	0	GAGACA (SEQ ID NO:112)	18	TGTATCGTATTACT ATGT (SEQ ID NO:113)	19	TTCGGGGAGTTA TTATAAC (SEQ ID NO:114)	2	GT	JH4B	-4 CTTTGA (SEQ ID NO:115)
1.6.1	A30	-3	TTACCC (SEQ ID 0	#n	N SEQ	Jk	# del	JK end			
1.6.1	A30	-3	TTACCC (SEQ ID 0	0		JK4	0	GCTCACT (SEQ ID			

1.6.2	A30	-3	TTACCC (SEQ ID NO:116)	0	0	JK4	0	GCTCACT (SEQ ID NO:117)
1.6.3	A30	-3	TTACCC (SEQ ID NO:116)	0	0	JK4	0	GCTCACT (SEQ ID NO:117)
1.11.1	A3/A19/DPK	-4	AAACTC (SEQ ID NO:118)	0	0	JK4	-2	TCACTTTC (SEQ ID NO:119)
1.11.2	A3/A19/DPK	-4	AAACTC (SEQ ID NO:118)	0	0	JK4	-2	TCACTTTC (SEQ ID NO:119)
1.23.1	A30	-3	TTACCC (SEQ ID NO:120)	0	0	JK1	0	GTGGAC (SEQ ID NO:120)
1.23.2	A30	-3	TTACCC (SEQ ID NO:120)	0	0	JK1	0	GTGGAC (SEQ ID NO:120)

FIGURE 43

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.17.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.3	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.18	DP-15/1-8	1	CGAGAG (SEQ ID NO:125)	1	A	D6-19	19	GGGTATAG CAGTGGCT GG (SEQ ID NO:126)	4	GACA	JH6B	-2	TACTAC (SEQ ID NO:127)
1.24.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.24.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.25.1	DP-73/5-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTATTATA TGGTTGG AGACTTATT ATAA (SEQ ID	3	TGT	JH4B	-4	CTTTGA (SEQ ID NO:135)

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.25.2	DP-73/5-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTATTTA TGTTTCGG AGACTTATT ATAA (SEQ ID NO:133)	3	TGT	JH4B	-4	CTTTGA (SEQ ID NO:134)
1.29	DP-73/5-51	0	GAGACA (SEQ ID NO:135)	1	C	D5-12	21	GTGGATGT AGGGGCT ACGATT (SEQ ID NO:136)	7	GGGGAT (SEQ ID NO:137)	JH6B	0	ATTACTAC (SEQ ID NO:138)
1.33	DP-14/1-18	0	GAGAGA (SEQ ID NO:139)	2	TC	D21-9	18	ATTACTAT GATAGTAG TG (SEQ ID NO:140)	7	ATTATCT (SEQ ID NO:141)	JH6B	-4	CTACTA (SEQ ID NO:142)
1.38.1	DP-50/3-33	1	CGAGAG (SEQ ID NO:143)	2	GA	D21-9	19	TATTACTA TGATAGTA GTG (SEQ ID NO:144)	7	ATTATCT (SEQ ID NO:145)	JH6B	-4	CTACTA (SEQ ID NO:146)
1.39.1	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT ATaaTTCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:150)
1.39.2	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT ATaaTTCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:150)
1.40.1	DP-15/1-8	1	CGAGAG (SEQ ID NO:148)	0	0	D2	25	ATATTGTA GTGGTGGT	2	CA	JH6B	-6	ACTACT (SEQ ID NO:149)

Clone #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
			NO:151)										NO:153)
1.40.2	DP-15/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:152)	2	CA	JH6B	-6	ACTACT (SEQ ID NO:153)
1.45	DP-15/1-8	0	GAGAGG (SEQ ID NO:154)	2	CA	DK4	20	GTGGATAC AGCTATGG TTAC (SEQ ID NO:155)	1	G	JH6B	-6	ACTACT (SEQ ID NO:156)
1.46.1	DP-15/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GT GGTGGTA GCTGCTAC (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.46.2	DP-15/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.48.1	DP-14/1-18	1	CGAGAG (SEQ ID NO:160)	7	TGTGAA (SEQ ID NO:161)	D21-9	20	TATTACTA TGATggTA GTGGTTAT (SEQ ID NO:162)	1	T	JH4B	0	ACTACT (SEQ ID NO:163)
1.48.2	DP-14/1-18	1	CGAGAG (SEQ ID NO:160)	7	TGTGAA (SEQ ID NO:161)	D21-9	20	TATTACTA TGATggTA GTGGTTAT (SEQ ID	1	T	JH4B	0	ACTACT (SEQ ID NO:163)

CLONE #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	#N's	N Sequence	JH	# del	JH Segment
1.49.1	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATA G TGGCTACG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.49.2	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATA G TGGCTACG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.51.1	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATT A CGTTTGa GGAattAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-5	TGGTTC (SEQ ID NO:171)
1.51.2	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATT A CGTTTGa GGAattAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-5	TGGTTC (SEQ ID NO:171)

CLONE	VK	#del	VK end	#n	N SEQ	JK	# del	JK end
1.17.1	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.17.2	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.17.3	A30	3	TTACCC (SEQ ID	0	0	JK4	0	GCTCACT (SEQ ID

CLONE	V _K	#del	V _K end	#n	N SEQ	J _K	# del	J _K end
1.18	A30	3	TTACCC (SEQ ID NO:174)	0	0	JK3	0	ATTACAC (SEQ ID NO:175)
1.24.1	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.24.2	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.25.1	A30	3	TTACCC (SEQ ID NO:178)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.25.2	A30	3	TTACCC (SEQ ID NO:178)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.29	A3/A19/DPK	7	CTACAA (SEQ ID NO:180)	14	TCTCTCATG TGCAG (SEQ ID NO:181)	JK2	-7	TTTGG (SEQ ID NO:182)
1.33	A20/DPK4	3	TGCCCC (SEQ ID NO:183)	0	0	JK4	0	GCTCAC (SEQ ID NO:184)
1.38.1	A20/DPK4	3	TGCCCC (SEQ ID NO:185)	0	0	JK1	0	GTGGAC (SEQ ID NO:186)
1.39.1	A30	3	TTACCC (SEQ ID NO:187)	0	0	JK1	0	GTGGAC (SEQ ID NO:188)
1.39.2	A30	3	TTACCC (SEQ ID NO:187)	0	0	JK1	0	GTGGAC (SEQ ID NO:188)
1.45	A20/DPK4	3	TGCCCC (SEQ ID NO:189)	0	0	JK3	0	ATTACAC (SEQ ID NO:190)
1.46.1	A30	0	CCCTCC (SEQ ID	0	0	JK1	-3	GACGTT (SEQ ID

CLONE	V _K	#del	V _K end	#n	N SEQ	J _K	# del	J _K end
1.46.2	A30	0	CCCTCC	0	0	JK1	-3	NO:192)
			(SEQ ID					GACGTT
			NO:191)					(SEQ ID
								NO:192)
1.48.1	L5/DPK5/V	1	TCCCTC	0	0	JK1	-2	GGACGTT
			(SEQ ID					(SEQ ID
			NO:193)					NO:194)
1.48.2	L5/DPK5/V	1	TCCCTC	0	0	JK1	-2	GGACGTT
			(SEQ ID					(SEQ ID
			NO:193)					NO:194)
1.49.1	A3/A19/DPK	5	CAAAC	0	0	JK5	-1	ATCACC
			(SEQ ID					(SEQ ID
			NO:195)					NO:196)
1.49.2	A3/A19/DPK	5	CAAAC	0	0	JK5	-1	ATCACC
			(SEQ ID					(SEQ ID
			NO:195)					NO:196)
1.51.1	A27/A27A	4	GCTCAC	1	T	JK3	0	ATTCAC
			(SEQ ID					(SEQ ID
			NO:197)					NO:198)
1.51.1	A27/A27A	4	GCTCAC	1	T	JK3	0	ATTCAC
			(SEQ ID					(SEQ ID
			NO:197)					NO:198)

FIGURE 44

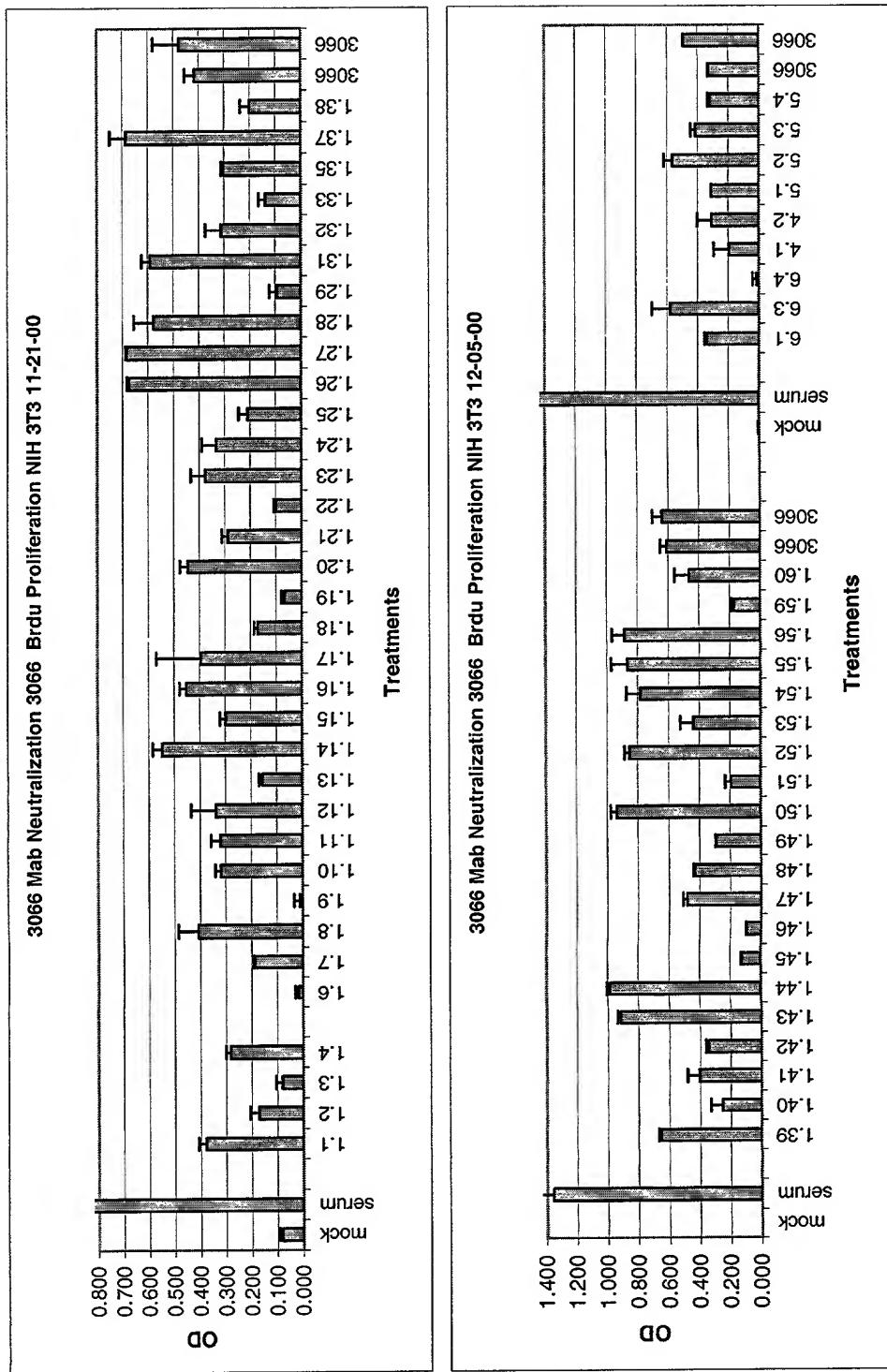


FIGURE 45

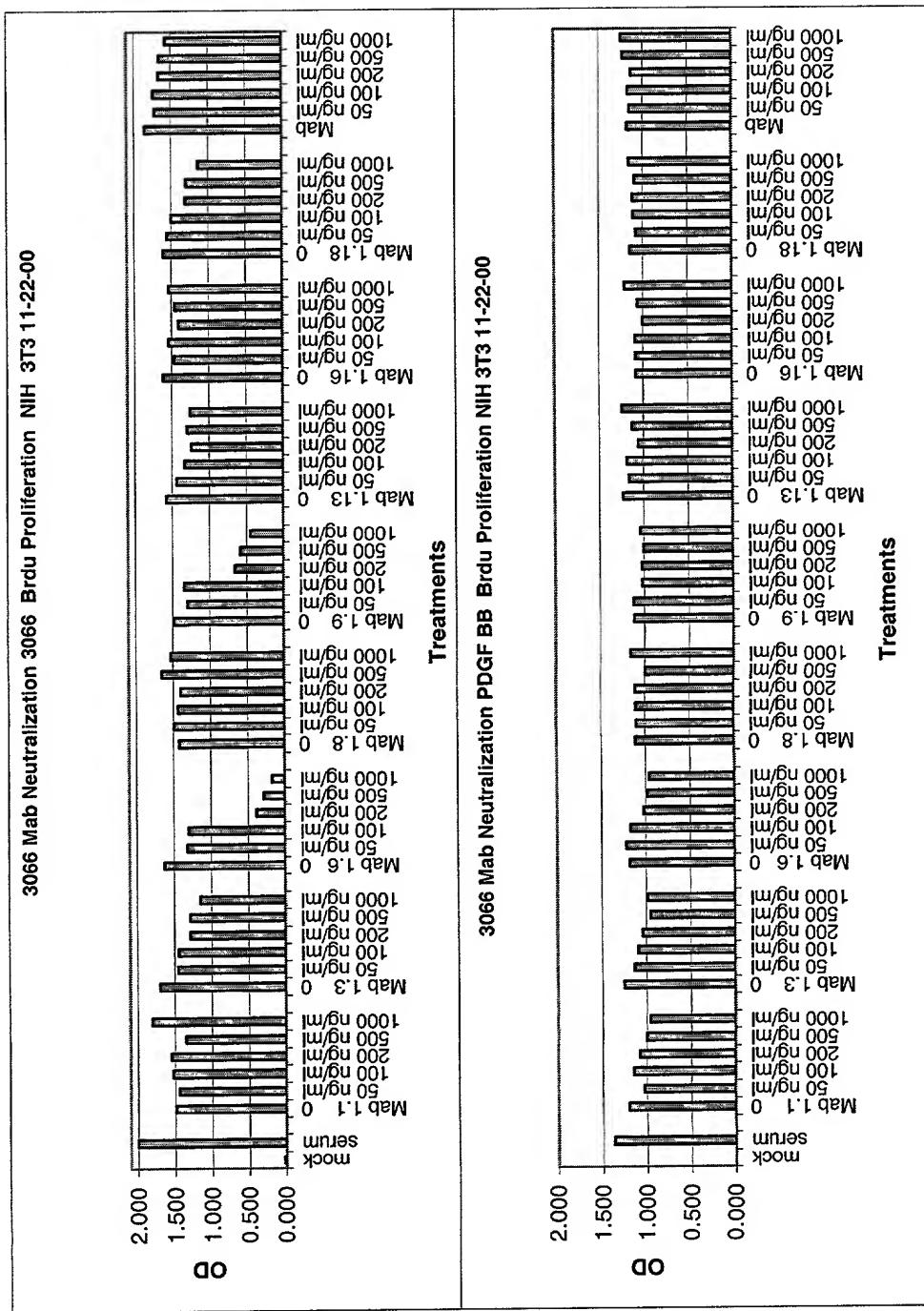


FIGURE 46

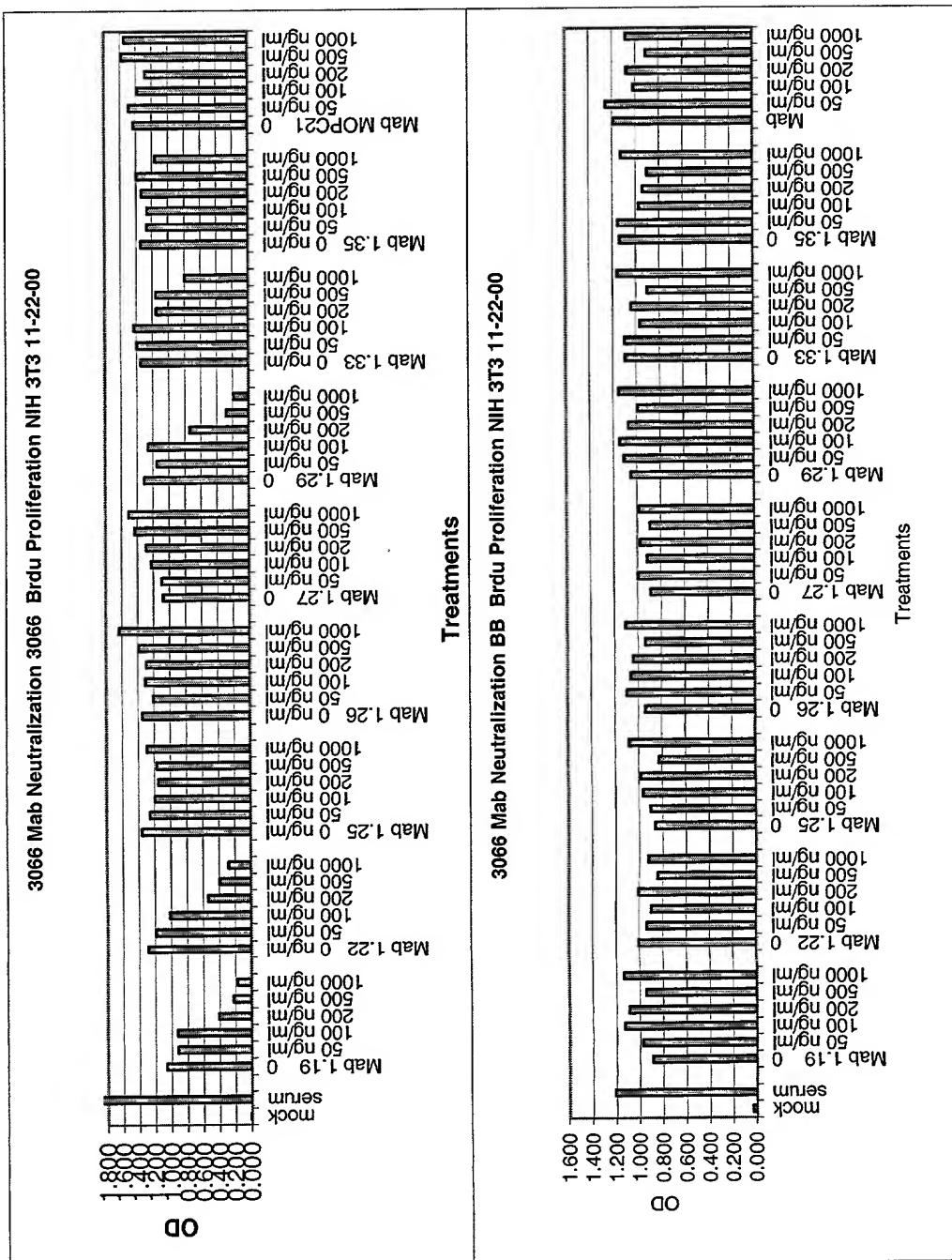


FIGURE 47

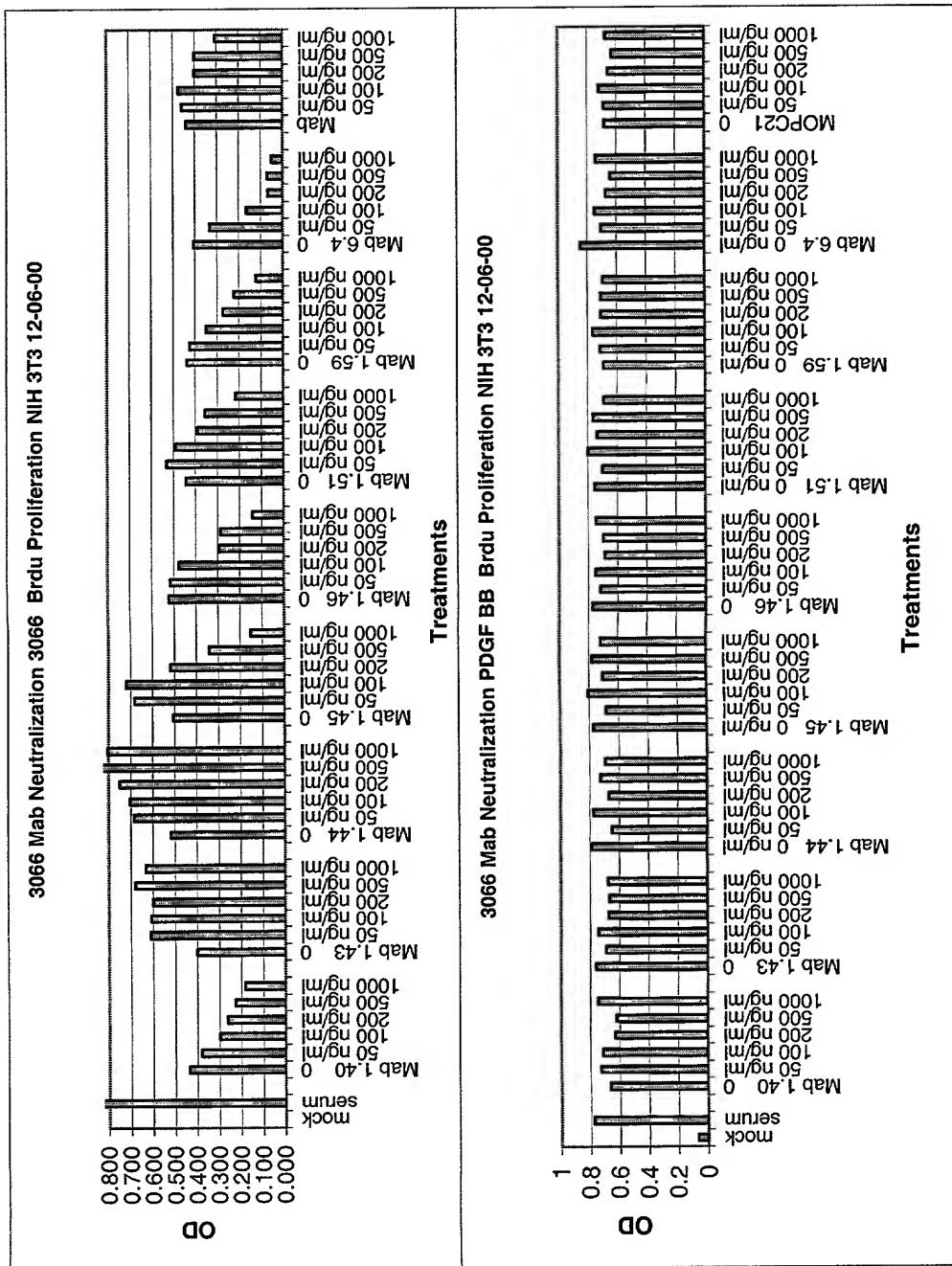


FIGURE 48

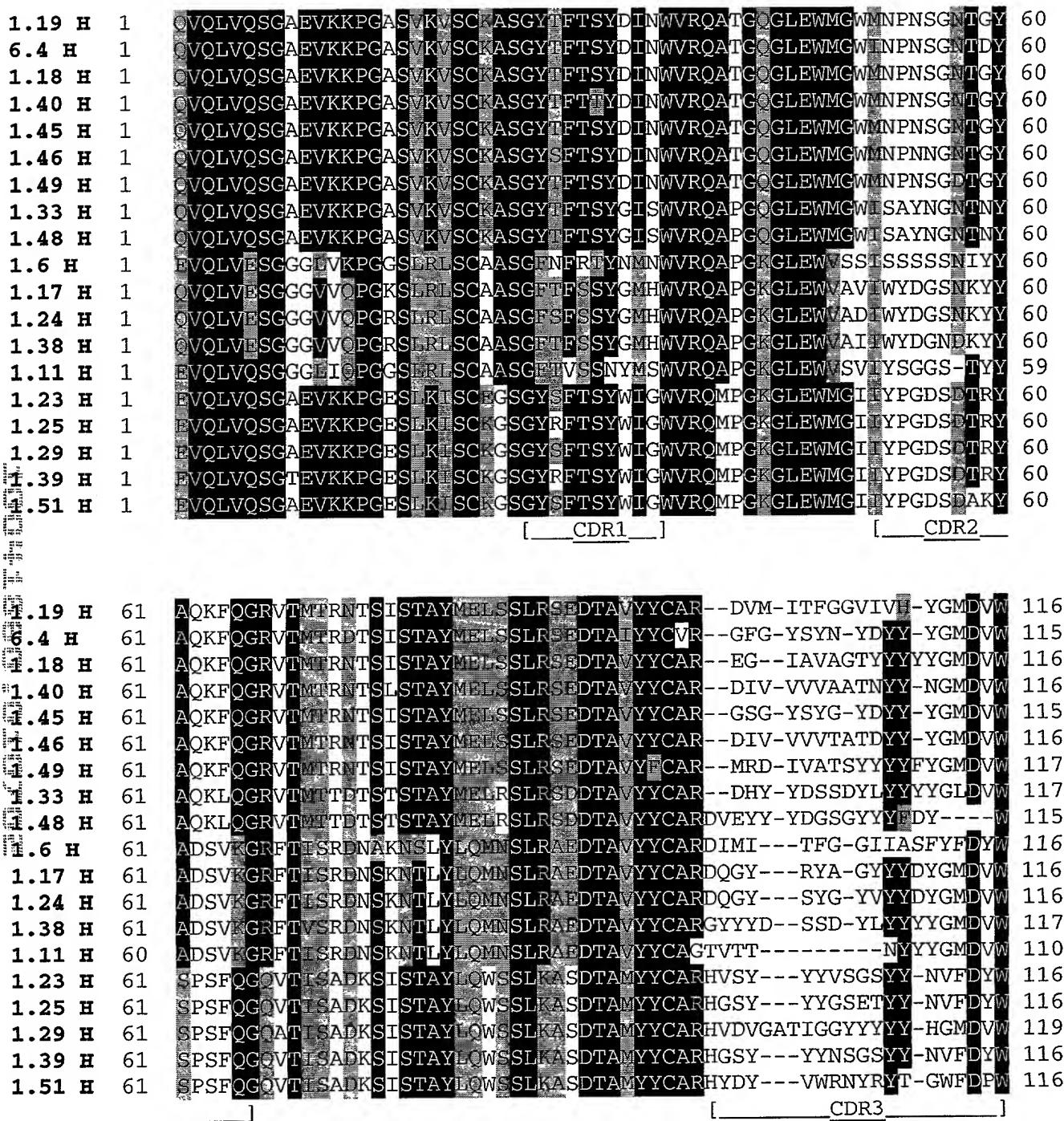


FIGURE 48 (CONT)

1.19 H	117	GQGTTVTVSS	126
6.4 H	116	GQGTTVTVSS	125
1.18 H	117	GQGTTVTVSS	126
1.40 H	117	GQGTTVTVSS	126
1.45 H	116	GQGTTVTVSS	125
1.46 H	117	GQGTTVTVSS	126
1.49 H	118	GQGTTVTVSS	127
1.33 H	118	GQGTTVTVSS	127
1.48 H	116	GQGTLVTVSS	125
1.6 H	117	GQGTLVTVSS	126
1.17 H	117	GQGTTVTVSS	126
1.24 H	117	GQGTTVTVSS	126
1.38 H	118	GQGTTVTVSS	127
1.11 H	111	GQGTTVTVSS	120
1.23 H	117	GQGTLVTVSS	126
1.25 H	117	GQGTLVTVSS	126
1.29 H	120	GQGTTVTVSS	129
1.39 H	117	GQGTLVTVSS	126
1.51 H	117	GQGTLVTVSS	126

FIGURE 49

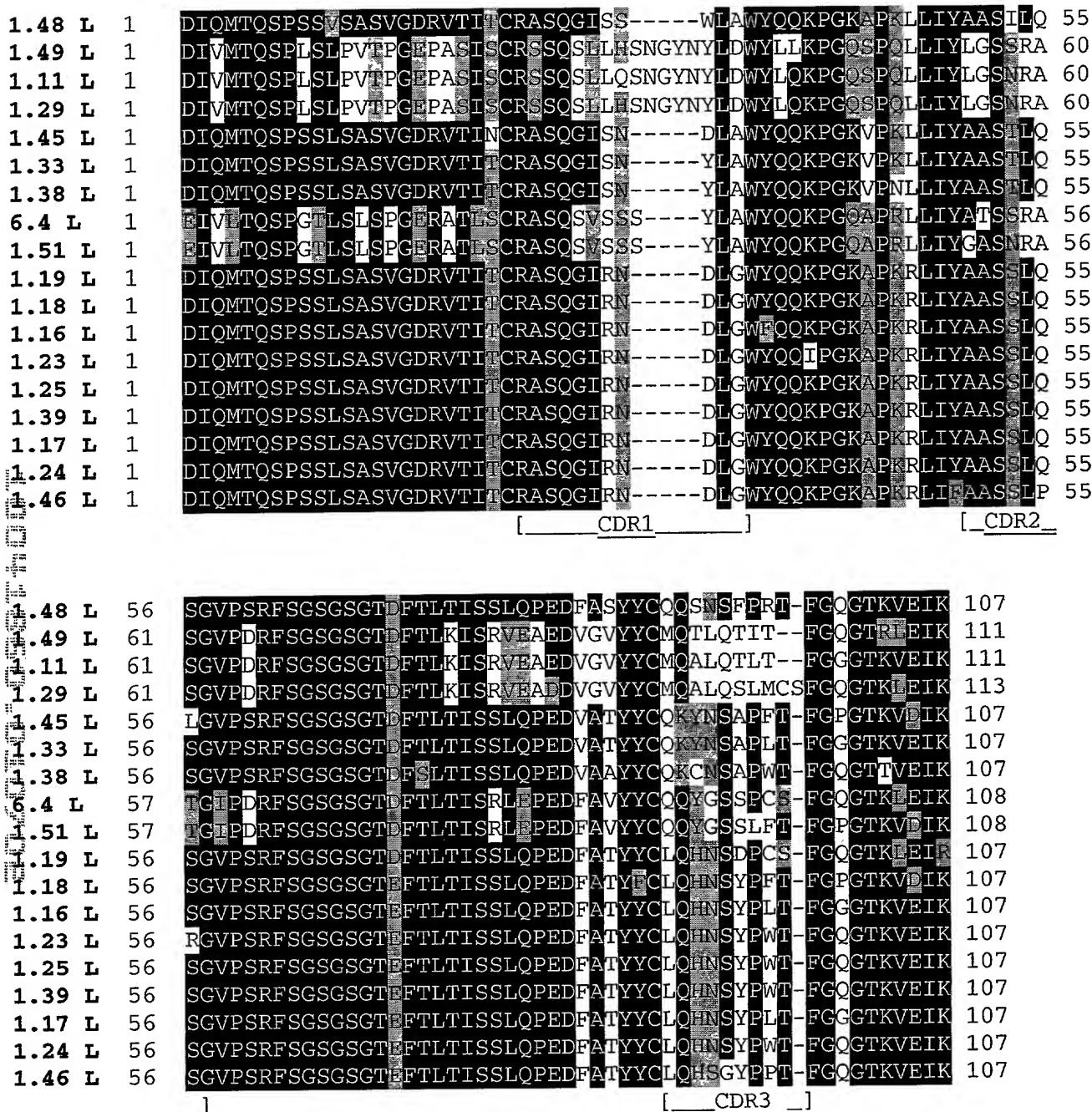


FIGURE 50

1.19 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY	60
6.4 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY	60
1.18 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY	60
1.40 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY	60
1.45 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY	60
1.46 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY	60
1.49 H	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY	60
		[CDR1]	[CDR2]
1.19 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGG-VIVHYGMDVWGQG	119
6.4 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCVRGFGYSYN--YDYYYYGMDVWGQG	118
1.18 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAGT-YYYYYNGMDVWGQG	119
1.40 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVAA-TNYYNGMDVWGQG	119
1.45 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSYG--YDYYYYGMDVWGQG	118
1.46 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVTA-TDYYYYGMDVWGQG	119
1.49 H	61	AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYCARMRDIVATSYYYYNGMDVWGQG	120
		[CDR3]	
1.19 H	120	TTVTVSS 126	
6.4 H	119	TTVTVSS 125	
1.18 H	120	TTVTVSS 126	
1.40 H	120	TTVTVSS 126	
1.45 H	119	TTVTVSS 125	
1.46 H	120	TTVTVSS 126	
1.49 H	121	TTVTVSS 127	

FIGURE 51

1.33 H 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60
1.48 H 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60
[CDR1] [CDR2]

1.33 H 61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR--DIYYDSSDYLYYGLDVWG 118
1.48 H 61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEYYDGSYYYEDY---WG 116
[CDR3]

1.33 H 119 QGTLTVVSS 127
1.48 H 117 QGTLTVVSS 125

FIGURE 52

1.17 H 1 QVQLVESGGVVQPGKSLRLSCAASGFFFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60
1.24 H 1 QVQLVESGGVVQPGKSLRLSCAASGFFSFSSYGMHWVRQAPGKGLEWVADIWYDGSNKYY 60
1.38 H 1 QVQLVESGGVVQPGKSLRLSCAASGFFFSSYGMHWVRQAPGKGLEWVAIIWYDGSNKYY 60
[CDR1] [CDR2]

1.17 H 61 ADSVKGRFTTSRDNSKNTLYLQMNSLRAEDTAVYYCARDQGY-RYAGYYYDYGMDVWGQG 119
1.24 H 61 ADSVKGRFTTSRDNSKNTLYLQMNSLRAEDTAVYYCARDQGY-SYGYVYYDYGMDVWGQG 119
1.38 H 61 ADSVKGRFTTSRDNSKNTLYLQMNSLRAEDTAVYYCARGYYYDSSDYLYYYYGMDVWGQG 120
[CDR3]

1.17 H 120 TTVTVSS 126
1.24 H 120 TTVTVSS 126
1.38 H 121 TTVTVSS 127

FIGURE 53

1.23 H 1 EVQLVQSGAEVKKPGESLKISCEGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDS DTRY 60
1.25 H 1 EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPGDS DTRY 60
1.29 H 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDS DTRY 60
1.39 H 1 EVQLVQSGTEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPGDS DTRY 60
1.51 H 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDS DAKY 60

[CDR1]

[CDR2]

1.23 H 61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHVSYYVSG---SYYNVFDYWG 117
1.25 H 61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSYYGSE---TYYNVFDYWG 117
1.29 H 61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYHGM DVWG 120
1.39 H 61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSYYNSG---SYYNVFDYWG 117
1.51 H 61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHYDYYWRNY---RYTGWFDPWG 117

[CDR3]

[CDR3]

1.23 H 118 QGTLVTVSS 126
1.25 H 118 QGTLVTVSS 126
1.29 H 121 QGTTVTVSS 129
1.39 H 118 QGTLVTVSS 126
1.51 H 118 QGTLVTVSS 126

1.23 1.25 1.29 1.39 1.51

FIGURE 54

1.49 L 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLDWYLLKPGQSPQLLIYLGS**SRA** 60
1.11 L 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLQSNGNYLDWYLLQKPGQSPQLLIYLGS**RA** 60
1.29 L 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLDWYLLQKPGQSPQLLIYLGS**RA** 60

[CDR1] [CDR2]

1.49 L 61 SGVPDRFSGSGSGTDFTLKISRVEA**DVGVYYCMQTLQ**~~IT~~**FGQGTRLEIK** 111
1.11 L 61 SGVPDRFSGSGSGTDFTLKISRVEA**DVGVYYCMQALQ**~~IT~~**FGGGTKEIK** 111
1.29 L 61 SGVPDRFSGSGSGTDFTLKISRVEA**DVGVYYCMQALQSLMCSFGQGTRLEIK** 113

[CDR3]

FIGURE 55

1.45 L 1 DTQMTQSPSSLSASVGDRVТИC~~RASQG~~ISNDLAWYQQKPGKVPK~~LLI~~YAASTLQLGVPS 60
1.33 L 1 DIQMTQSPSSLSASVGDRVТИC~~RASQG~~ISNYLAWYQQKPGKVPK~~LLI~~YAASTLQSGVPS 60
1.38 L 1 DIQMTQSPSSLSASVGDRVТИC~~RASQG~~ISNYLAWYQQKPGKVPN~~LLI~~YAASTLQSGVPS 60

[CDR1] [CDR2]

1.45 L 61 RFSGSGSGTDF~~S~~LTISSLQPEDVATYYCQKYNSAPFTFGPGTKV~~D~~IK 107
1.33 L 61 RFSGSGSGTDF~~S~~LTISSLQPEDVATYYCQKYNSAPLTFGGGT~~K~~V~~E~~IK 107
1.38 L 61 RFSGSGSGTDF~~S~~LTISSLQPEDVA~~Y~~YCQKCNSAPWTFGQGTT~~V~~~~E~~IK 107

[CDR3]

FIGURE 56

6.4 L 1 EIVLTQSPGTLSSLPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
1.51 L 1 EIVLTQSPGTLSSLPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASN RATGIP 60
[CDR1] [CDR2]

6.4 L 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFQGTTKLEIK 108
1.51 L 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSLFVFGPGTKVDIK 108
[CDR3]

FIGURE 57

1.19 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.18 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.16 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.23 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQIPGKAPKRLIYAASSLQSGVPS	60
1.25 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.39 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.17 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.24 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS	60
1.46 L	1	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIAASSLPSGVPS	60

[CDR1]

[CDR2]

1.19 L	61	RFSGSGSGT D FTLTISSLQPEDFATYYCLQHNSDPC S FGQG T K E I R	107
1.18 L	61	RFSGSGSGTEFTLTISSLQPEDFATY D CLQHNSYPFTFGPGTKV D I K	107
1.16 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGT K VEIK	107
1.23 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSY P WTFGQG T K V EIK	107
1.25 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQG T K V EIK	107
1.39 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSY P WTFGQG T K V EIK	107
1.17 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGT K VEIK	107
1.24 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSY P WTFGQG T K V EIK	107
1.46 L	61	RFSGSGSGTEFTLTISSLQPEDFATYYCLQHSGY P TFGQG T K V EIK	107

[CDR3]

1.19 1.18 1.16 1.23 1.25 1.39 1.17 1.24 1.46